OM nucleic - nucleic search, using sw model

GenCore version 5.1.9
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Run on: June 16, 2006, 23:29:06 ; Search time 837 Seconds
(without alignments)
10995.661 Million cell updates/sec

Title: US-10-521-428A-1
Perfect score: 1320
Sequence: 1 atgaagtcgatcctagatgg............cgtctgccgaggcctgtga 1320
Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0
Searched: 5244920 seqs, 3486124231 residues
Total number of hits satisfying chosen parameters: 10489840
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqm2001as:*
5: geneseqm2001bs:*
6: geneseqm2002as:*
7: geneseqm2002bs:*
8: geneseqm2003aa:*
9: geneseqm2003bs:*
10: geneseqm2003cs:*
11: geneseqm2004aa:*
12: geneseqm2004bs:*
13: geneseqm2005as:*
14: geneseqm2005bs:*
15: geneseqm2006s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1320	100.0	1320	12	ADM82793	Adm82793 Human can
2	1259.4	95.4	5665	10	ADL15026	Adl15026 Human CB1
3	1259.4	95.4	5665	15	AEE18784	Aee18784 Human CB1
4	1257.8	95.3	1419	12	ACH91680	Ach91680 Human gen
5	1257.8	95.3	1507	2	AAQ14003	Aaq14003 Human can
6	1257.8	95.3	1755	8	ABZ42646	Abz42646 Human can
7	1257.8	95.3	1755	11	ADN38917	Adn38917 Cancer/an
8	1257.8	95.3	5471	13	ACN38515	Acn38515 Tumour-as
9	1257.8	95.3	5480	14	ABA81160	Aea81160 Human can
10	1257.8	95.3	5653	9	ADA24536	Ada24536 Human cDN
11	1256.2	95.2	1419	12	ADH77049	Adh77049 hCB-1 dou
12	1256.2	95.2	1419	12	ADH77050	Adh77050 hCB-1-D21
13	1256.2	95.2	1419	12	ADO29849	Ado29849 Human GPC
14	1256.2	95.2	2135	6	ABZ35604	Abz35604 Human gen
15	1256.2	95.2	2135	10	ACA56852	Aca56852 Human sig
16	1256.2	95.2	2135	10	ACC72645	Acc72645 Human sig
17	1256.2	95.2	2135	11	ADI32143	Adi32143 Human cDN
18	1256.2	95.2	2135	12	ADI56648	Adi56648 Human pol
19	1256.2	95.2	2135	13	ADS84210	Ads84210 Human lym
20	1256.2	95.2	5651	6	ABZ35298	Abz235298 Human gen
21	1254.6	95.0	1419	6	ABI97974	Abi97974 Non-endog
22	1254.6	95.0	1419	12	ADH77051	Adh77051 hCB-1-D38
23	1251.4	94.8	5472	11	ADN38919	Adn38919 Cancer/an
24	1209.8	91.7	1551	6	ABK34744	Abk34744 Human cDN
25	1151	87.2	1252	11	ADN38921	Adn38921 Cancer/an
26	1151	87.2	1252	11	AEA81161	Aea81161 Human can
27	1077.4	81.6	2370	13	ADU82909	Adu82909 Ligand up
28	1048	79.4	1423	12	ADO30140	Ado30140 Mouse GPC
29	1048	79.4	1654	6	ABI99249	Abi99249 Mouse 18c
30	795.8	60.3	993	14	ABI99249	Abi99249 Mouse GPC
31	506.2	38.3	600	14	AAI72354	Aai72354 CB2R gene
32	498.4	37.8	500	12	ADO30141	Ado30141 Mouse GPC
33	252.4	19.1	3715	6	AEE11326	Aee11326 Hamster c
34	252.4	19.1	3715	12	AEE14968	Aee14968 Hamster S
35	252.4	19.1	3715	12	ACH77959	Ach77959 Human gen
36	252.4	19.1	3715	12	ADQ97951	Adq97951 Mouse can
37	246.8	18.7	1906	12	ADQ97954	Adq97954 Human can
38	246.8	18.7	21906	12	ADQ97955	Adq97955 Mouse can
39	246.4	18.7	21906	15	AEE18785	Aee18785 Human CB2
40	245.2	18.6	1083	12	ADO29850	Ado29850 Human GPC
41	245.2	18.6	1083	14	ADV43994	Adv43994 Human psy
42	245.2	18.6	1776	8	ABZ42647	Abz42647 Human can
43	245.2	18.6	1790	2	AAQ74797	Aaq74797 Cannabino
44	245.2	18.6	1790	10	ACA56761	Aca56761 Human sig
45	245.2	18.6	1790	11	ADI32072	Adi32072 Human cDN

ALIGNMENTS

RESULT 1
ADM82793

ID   ADM82793 standard; cDNA; 1320 BP.
XX
AC   ADM82793;
XX
DT   03-JUN-2004 (first entry)
XX
DE   Human cannabinoid 1 receptor splice variant CB1b-encoding cDNA.
XX
KW   Human; CB1 receptor; splice variant; cannabinoid 1 receptor;
KW   CB1 receptor; drug screening; cannabinoid receptor-associated disorder;
KW   obesity; pain; psychiatric disorder; depression; anxiety;
KW   neurological disorder; Parkinson's disease; Alzheimer's disease;
KW   anorectic; analgesic; neuroleptic; antidepressant; tranquilliser;
KW   antiparkinsonian; neuroprotective; nootropic; gene therapy; gene; ss.
XX
OS   Homo sapiens.
XX
FH
FH   Key   Location/Qualifiers
FT
FT   CDS   1..1320
FT   /*tag= a
FT   /product= "CB1b receptor"
XX
PN   WO2004007551-A1.
XX
PD   22-JAN-2004.
XX
PF   14-JUL-2003; 2003WO-GB003067.
XX
PR   17-JUL-2002; 2002SE-00002240.
XX
PA   (ASTR) ASTRAZENECA AB.
PA   (ASTR) ASTRAZENECA UK LTD.
XX
PI   Vu HK, Groblewski T, Greasley P;
XX
DR   WPI; 2004-1228492/12.
DR   P-PSDB; ADM82794.
XX
PT   New human cannabinoid (CB) 1b receptor polypeptides and nucleic acid

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PT   molecules, useful for diagnosing, preventing or treating CB-associated
PT   disorders e.g. obesity, pain, anxiety or neurological disorders and in
PT   drug screening.
XX
PS   Claim 1; SEQ ID NO 1; 34pp; English.
XX
CC   The invention relates to a novel splice variant, CB1b (ADM82794), of the
CC   human cannabinoid 1 (CB1) receptor and nucleic acids encoding it
CC   (ADM82793). Compared with the known CB1 receptor, the CB1b receptor has a
CC   deletion of 33 residues towards the N-terminus (residues 22-54 of the CB1
CC   receptor). The invention also relates to sequences at least 95% identical
CC   to the CB1b receptor nucleic acid and protein sequences of the invention;
CC   vectors and host cells comprising a CB1b receptor nucleic acid sequence;
CC   a method for the recombinant production of the CB1b receptor; a method of
CC   detecting a CB1b receptor nucleic acid; methods of screening or
CC   identifying compounds which bind to the CB1b receptor; CB1b receptor
CC   agonists, antagonists, inverse agonists or modulators and pharmaceutical
CC   compositions containing them; and methods of treating or preventing a
CC   disorder associated with cannabinoid receptors. The pharmaceutical
CC   compositions and methods of the invention are useful in diagnosing,
CC   preventing or treating CB receptor-associated disorders such as obesity,
CC   pain, psychiatric disorders (e.g. depression or anxiety) or neurological
CC   disorders (e.g. Parkinson's disease or Alzheimer's disease). The present
CC   sequence represents cDNA encoding the human CB1b receptor.
XX
SQ   Sequence 1320 BP; 291 A; 386 C; 335 G; 308 T; 0 U; 0 Other;

Query Match             100.0%;  Score 1320;  DB 12;  Length 1320;
Best Local Similarity   100.0%;
Matches 1320;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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Qy         1 ATGAAGTCGATCCTAGATGGCCTTGCAGATAACCACCACTTCCGGGACCATCACCACTGACCTC 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 ATGAAGTCGATCCTAGATGGCCTTGCAGATAACCACCACTTCCGGGACCATCACCACTGACCTC 60

Qy        61 CTGGGAAGTCCCTTCCAAGAGAAGAAGATGACTGCGGGAGACAACCCAGCTAGTCCCAGCA 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 CTGGGAAGTCCCTTCCAAGAGAAGAAGATGACTGCGGGAGACAACCCAGCTAGTCCCAGCA 120

Qy       121 GACCAGGTGAACATTACAGAGAATTTTACAACAAGTCTCTCTCCTTCCTTCAAGAGAATGAG 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 GACCAGGTGAACATTACAGAGAATTTTACAACAAGTCTCTCTCCTTCCTTCAAGAGAATGAG 180

Qy       181 GAGAACAATCCAGTGTGGGGAGGAGAACTTCATGGACAATAGAGTGTTTCATGGTCTGAACCCC 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 GAGAACAATCCAGTGTGGGGAGGAGAACTTCATGGACAATAGAGTGTTTCATGGTCTGAACCCC 240

Qy       241 AGCCAGCAGCTGCCCATTGCAGTCCTGTCCCTCGCTGGGCACACTTCACGGTGTCCTGGAG 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 AGCCAGCAGCTGCCCATTGCAGTCCTGTCCCTCGCTGGGCACACTTCACGGTGTCCTGGAG 300

Qy       301 AACCTCCTGGTTGCTGCGTGCGTCATCCTCCACTCCGCCCTCGGCTGGCCTTCCTTCTAC 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 AACCTCCTGGTTGCTGCGTGCGTCATCCTCCACTCCGCCCTCGGCTGGCCTTCCTTCTAC 360

Qy       361 CACTTCATCGGCCAGCCTGGCCGGTGGCAGGACCTTCCAGACTTCATTTTTGTCTACAGC 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 CACTTCATCGGCCAGCCTGGCCGGTGGCAGGACCTTCCAGACTTCATTTTTGTCTACAGC 420

Qy       421 TTCATTGACTTCCACGTGTTCCACCGCCAAAGATAGCCCACCGTGTTTCGTTCAAACTG 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 TTCATTGACTTCCACGTGTTCCACCGCCAAAGATAGCCCACCGTGTTTCGTTCAAACTG 480

Qy       481 GGTGGGGTCACGGCCTCCTTCACTGCCTCCGTGGGCAGCCTGTTCCTCACAGCCATCGAC 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 GGTGGGGTCACGGCCTCCTTCACTGCCTCCGTGGGCAGCCTGTTCCTCACAGCCATCGAC 540

Qy       541 AGGTACATATCCATTCACAGGCCCCTGCCTAAGAGGAATTGTCACCAGGCCCCAAGGCC 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 AGGTACATATCCATTCACAGGCCCCTGCCTAAGAGGAATTGTCACCAGGCCCCAAGGCC 600

Qy       601 GTGGTAGCGGTTTTGCCTGATGTGGACCATAGCCATTGTGATCGGCCGTGCTGCCTCCTG 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 GTGGTAGCGGTTTTGCCTGATGTGGACCATAGCCATTGTGATCGGCCGTGCTGCCTCCTG 660
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Db       601 GGCTGGGAACTGCCAGAAAACTGCAAATCTGTTTGCTCAGACATTTTCCCACACATTGATGAA 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       661 GGCTGGGAACTGCCAGAAAACTGCAAATCTGTTTGCTCAGACATTTTCCCACACATTGATGAA 720

Db       721 ACCTACCTGATGTTCTGGATCGGGGTGACCAGCGTACTGCTTCTGTTCATCGTGTATGCG 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       721 ACCTACCTGATGTTCTGGATCGGGGTGACCAGCGTACTGCTTCTGTTCATCGTGTATGCG 780

Db       781 TACATGTATATTCTCTGGAAGGCTCACAGCCACAGCGTCCGCAGTGATTCAGGGGACC 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       781 TACATGTATATTCTCTGGAAGGCTCACAGCCACAGCGTCCGCAGTGATTCAGGGGACC 840

Db       841 CAGAGAGAGCATCATCCACACGTCTGAGGATGGGAAGGTACAGGTGAACCGGCCAGAC 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       841 CAGAGAGAGCATCATCCACACGTCTGAGGATGGGAAGGTACAGGTGAACCGGCCAGAC 900

Db       901 CAAGCCCGCATGGACATTAGGTTAGCCAAGACCCTGGTCCTGATCCTGGTGGTTGATC 960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       901 CAAGCCCGCATGGACATTAGGTTAGCCAAGACCCTGGTCCTGATCCTGGTGGTTGATC 960

Db       961 ATCTGCTGGGGGCCCTCTGCTTGGCAATCATGGGTGTATGCAGAAGATGAATGTCTTTGGGAAGAATGAACAAG 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       961 ATCTGCTGGGGGCCCTCTGCTTGGCAATCATGGGTGTATGCAGAAGATGAATGTCTTTGGGAAGAATGAACAAG 1020

Db      1021 CTCATTAAGACGGTGTTTGCATTCTGCAGTATGCTTCTGGCCTGCTGAACTCACCGTGGAAC 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      1021 CTCATTAAGACGGTGTTTGCATTCTGCAGTATGCTTCTGGCCTGCTGAACTCACCGTGGAAC 1080

Db      1081 CCCATCATCTATGCTCTCAGGAGTAAGGACCTGGCGACACGCGTTTCCGGAGCATGTTTCCC 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      1081 CCCATCATCTATGCTCTCAGGAGTAAGGACCTGGCGACACGCGTTTCCGGAGCATGTTTCCC 1140

Db      1141 TCTTGTGAAGGCACTGGCGCAGCCTCTCGGATAACAGCAGCATGGGGGGACTGCCCTGCAC 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      1141 TCTTGTGAAGGCACTGGCGCAGCCTCTCGGATAACAGCAGCATGGGGGGACTGCCCTGCAC 1200

Db      1201 AAACACGCAAACAAATGCAGCCCAGTGTTCACAGGGCCGGCAGAAAGCTGCATCAAGAGCACG 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      1201 AAACACGCAAACAAATGCAGCCCAGTGTTCACAGGGCCGGCAGAAAGCTGCATCAAGAGCACG 1260

Db      1261 GTCAAGATTGCCAAGGTAACCAATGTCTGTGTCCACAGACACGTCTGCGAGCCTCTGTGA 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      1261 GTCAAGATTGCCAAGGTAACCAATGTCTGTGTCCACAGACACGTCTGCGAGCCTCTGTGA 1320
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RESULT 2
ADI15026
ID    ADI15026 standard; DNA; 5665 BP.
XX
AC    ADI15026;
XX
DT    06-MAY-2004  (first entry)
XX
DE    Human cannbinoid receptor DNA for cancer treatment.
XX
KW    ds; gene; cytostatic; gene therapy; binding moiety; medicine; imaging;
KW    diagnosis; prognosis; mantle cell lymphoma; cancer.
XX
OS    Homo sapiens.
XX
PN    WO2003068268-A2.
XX
PD    21-AUG-2003.
XX
PF    13-FEB-2003;  2003WO-EP001461.
XX
PR    14-FEB-2002;  2002GB-00003480.
PR    29-JUN-2002;  2002GB-00015095.
XX
PA    (BIOI-) BIOINVENT INT AB.
XX
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PI   Ek S, Borrebaeck CAK, Ehinger M;
XX
DR   WPI; 2003-697496/66.
DR   P-PSDB; AD115025.
XX
PT   New compound for treating, imaging, diagnosing or prognosing mantle cell
PT   lymphoma, comprises a binding moiety (e.g. antibody) that binds to a
PT   protein (e.g. human autotaxin polypeptide), and a further moiety (e.g.
PT   nucleic acid).
XX
PS   Disclosure; SEQ ID NO 38; 342pp; English.
XX
CC   The invention relates to a compound comprising a binding moiety which
CC   selectively binds to a protein or polypeptide listed in the specification
CC   (e.g. human autotaxin polypeptide or human CD24 signal transducer
CC   polypeptide), and a further moiety. The compound is useful in medicine or
CC   in the treatment, imaging, diagnosis or prognosis of mantle cell
CC   lymphoma (MCL). It is used in preparing a medicament for treating MCL, a
CC   diagnostic or prognostic agent for MCL, or an agent for imaging MCL cells
CC   in the body of an individual. This sequence corresponds to a gene
CC   encoding one of the polypeptides of the invention.
XX
SQ   Sequence 5665 BP; 1603 A; 1185 C; 1118 G; 1759 T; 0 U; 0 Other;

Query Match             95.4%;  Score 1259.4;  DB 10;  Length 5665;
Best Local Similarity   99.5%;  Pred. No. 0;
Matches 1263;   Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy         52 ACTGACCTCCTCGGGAGTCCCTTCCAAGAGAGAAGAGATGACTGGCGGGAGACAACCCCAGCTA 111
              |||||  |||| ||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        272 ACTTCCTTAGGGGAGAGTCCCTTCCAAGAGAGAGATGACTGGCGGGAGACAACCCCAGCTA 331

Qy        112 GTCCCAGCAGACCAGGTGAACATTACAGAATTTACAACAAGTCTCTCTGGTCCTTCAAG 171
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GTCCCAGCAGACCAGGTGAACATTACAGAATTTACAACAAGTCTCTCTGCCTTCAAG 391

Qy        172 GAGAATAGAGGAGAACATCCAGTGTGGGGAGAACTTCATGGACATAGACTGTTTCATGGTC 231
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 GAGAATAGAGGAGAACATCCAGTGTGGGGAGAACTTCATGGACATAGACTGTTTCATGGTC 451

Qy        232 CTGAACCCCAGCCAGCAGCTGGCCATTGGCAGTCCCGTCCCTCACGCTGGGCCACTTCACG 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 CTGAACCCCAGCCAGCAGCTGGCCATTGGCAGTCCCGTCCCTCACGCTGGGCCACTTCACG 511

Qy        292 GTCCTGGAGAACCTCCTGGTGCTGTGCCTCATCCTCCACTCCCGCCAGCCTCCGCTGCAGG 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        512 GTCCTGGAGAACCTCCTGGTGCTGTGCCTCATCCTCCACTCCCGCCAGCCTCCGCTGCAGG 571

Qy        352 CCTTCCTACCACTTCATCGGCAGCCTGGCCGTGGCAGACCTCCTGGGAGTGCATCATTTT 411
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        572 CCTTCCTACCACTTCATCGGCAGCCTGGCCGTGGCAGACCTCCTGGGAGTGCATCATTTT 631

Qy        412 GTCTACAGCTTCATTGACTTCCACGTGTTCCACCGTGGTGTTCG 471
              |||||||||||||||||||||||||||||||||||||||||||
Db        632 GTCTACAGCTTCATTGACTTCCACGTGTTCCACCGTGGTGTTCG 691

Qy        472 TTCAAACTGGGTGGGGTCACCGCCCTCCTTCACTGCCTCCGTTCCTTGTTCCTCACA 531
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        692 TTCAAACTGGGTGGGGTCACCGCCCTCCTTCACTGCCTCCGTTCCTTGTTCCTCACA 751

Qy        532 GCCATCGACACAGGTACATATATCCATTCACACGAGGACCCTGCCCTATAAGAGAGGATTGTCACCAGG 591
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 GCCATCGACACAGGTACATATTCACATTCACAGGAGGACCCTGCCCTATAAGAGAGGATTGTCACCAGG 811

Qy        592 CCCAAGCCGTGGTAGGGTTTTGCCTGAGTGTGGACCATAGCCATTGTGATCGGCGTGCTG 651
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        812 CCCAAGCCGTGGTAGGGTTTTGCCTGAGTGTGGACCATAGCCATTGTGATCGGCGTGCTG 871

Qy        652 CCTCTCCTGGGCTGGACTGCAGAAAACTGCAAATCTGTTTGCTCAGACATTTTCCCACAC 711
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        872 CCTCTCCTGGGCTGGACTGCAGAAAACTGCAAATCTGTTTGCTCAGACATTTTCCCACAC 931

Qy        712 ATTGATGAGAAACTACCTGATGTTCTGGATCGGGGATCGGGGGTCACCGTACTGCTTCTGTTCATC 771
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Db        932 ATTGATGAAAACTACCTGATGTTCTGGATCGGGGGTCACCGTACTGCTTCTGTTCATC 991
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy        772 GTGTATGCGTACATGTATATTCTTCGGGAGAGGCTCACAGCCACAGGCGTCCGCATGATTCAG 831
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        992 GTGTATGCGTACATGTATATTCTTCGGGAGAGGCTCACAGCCACAGGCGTCCGCATGATTCAG 1051

Qy        832 CGTGGCACCCAGAAGAGCATCATCATCCACACGTCTGAGGATGGAAGGTACCTGAGCACTCC 891
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1052 CGTGGCACCCAGAAGAGCATCATCATCCACACGTCTGAGGATGGAAGGTACCTGAGCACTCC 1111

Qy        892 CGGCCAGACCAAGCCCGCAATGGACAATTAAGGTTAGGCAAGAACCCTGGGTCCTTGGTG 951
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1112 CGGGCAGACCAAGCCCGCAATGGACAATTAAGGTTAGGCAAGAACCCTGGGTCCTTGGTG 1171

Qy        952 GTGTTGATCATCTGCTGGGGACCCCTCTTGCTTGCAAATCATGGTGTAGTCTTGGCTTGGGAAG 1011
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1172 GTGTTGATCATCTGCTGGGGACCCCTCTTGCTTGCAATCATGGTGTAGTCTTGGGAAG 1231

Qy       1012 ATGAACAAGCTCATTAAGACGGGTTTGCATTCTGACAGGATAGTTGCTTGTGAACTCC 1071
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1232 ATGAACAAGCTCATTAAGACGGGTTTGCATTCTGACAGGATAGTTGCTTGTGAACTCC 1291

Qy       1072 ACCGTGAACCCATCATCTATGCTCTGAGGAGTAAGGACCTGCCAGCACGCGTTCCGGACC 1131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1292 ACCGTGAACCCATCATCTATGCTCTGAGGAGTAAGGACCTGCCAGCACGCGTTCCGGAGC 1351

Qy       1132 ATGTTTCCCTCTTGTGAAGGCACTGGGGACACACCATGGGGGGTGGGGGGGGACTCGGAC 1191
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1352 ATGTTTCCCTCTTGTGAAGGCACTGGGGACACACCATGGGGGGTGGGGGGGGACTCGGAC 1411

Qy       1192 TGCCTGCACAAAACACGCAAACAATGCAGCCAGTGTTCACAGGGCCGCAGAAAAGCTGCATC 1251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1412 TGCCTGCACAAAACACGCAAACAATGCAGCCAGTGTTCACAGGGCCGCAGAAAAGCTGCATC 1471

Qy       1252 AAGAGCACGGTCAAGATTGCCAAGGTAACCATGTCTTGTGTCCACAGAGACACGTCTGCCGAG 1311
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1472 AAGAGCACGGTCAAGATTGCCAAGGTAACCATGTCTTGTGTCCACAGAGACACGTCTGCCGAG 1531

Qy       1312 GCTCTGTGA 1320
              |||||||||
Db       1532 GCTCTGTGA 1540
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RESULT 3
AEE18784
ID   AEE18784 standard; DNA; 5665 BP.
XX
AC   AEE18784;
XX
DT   26-JAN-2006  (first entry)
XX
DE   Human CB1 cannabinoid receptor gene (CNR1).
XX
KW   Diagnosis; pharmaceutical; therapeutic; osteoporosis;
KW   osteopathic; degeneration; endocrine disease; musculoskeletal disease;
KW   cannabinoid CB1; receptor; gene; chromosome 6; ds.
XX
OS   Homo sapiens.
XX
PN   US2005260608-A1.
XX
PD   24-NOV-2005.
XX
PF   24-MAY-2004; 2004US-00851667.
PR   24-MAY-2004; 2004US-00851667.
XX
PA   (ZIMM/) ZIMMER A.
PA   (KARS/) KARSAK M.
PA   (DVER/) DE VERNEUIL M.
PA   (BABI/) BAB I.
PA   (SHOH/) SHOHAMI E.
```

PA   (MECH/) MECHOULAM R.
XX
PI   Zimmer A, Karsak M, De Vernejoul M, Bab I, Shohami E;
PI   Mechoulam R;
XX
DR   WPI; 2006-008361/01.
DR   GENBANK; U73304.
XX
PT   Determining if an individual is predisposed to osteoporosis comprises
PT   detecting an osteoporosis-associated genotype, in a homozygous form.
PT   heterozygous form, in the CNR2 locus.
XX
PS   Example 3; SEQ ID NO 24; 39pp; English.
XX
CC   The present invention relates to a method of determining if an individual
CC   is predisposed to osteoporosis. The method involves detecting an
CC   osteoporosis-associated genotype, in a homozygous or heterozygous form,
CC   in the CNR2 locus encoding the cannabinoid receptor 2 (CB2) protein. The
CC   invention further provides identification of an osteoporosis risk
CC   haplotype using single nucleotide polymorphisms (SNPs) present in the
CC   CNR2 locus. The method, kit and pharmaceutical composition of the
CC   invention are useful for diagnosing, delaying onset of, preventing and
CC   treating osteoporosis. The present sequence is a human CB1 cannabinoid
CC   receptor gene (CNR1) which is located on human chromosome 6q14-q15.
XX
SQ   Sequence 5665 BP; 1603 A; 1185 C; 1118 G; 1759 T; 0 U; 0 Other;

Query Match   95.4%; Score 1259.4; DB 15; Length 5665;
Best Local Similarity   99.5%;
Matches 1263; Conservative   0; Mismatches   6; Indels   0; Gaps   0;
Pred. No.: 0;

```
Qy         52 ACTGAACCTCCTGGGGAAGTCCCTTCCAAGAGAAGATGACTGCGCGGAGACAACCCCAGCTA 111
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 ACTTCCTTTAGGGGAAGTCCCTTCCAAGAGAAGATGACTGCGCGGAGACAACCCCCAGCTA 331

Qy        112 GTCCCAGCAGACCAGGTGAACATTACAGAATTTTACACAGAGTCTCTCGTGCCTTCAAG 171
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GTCCCAGCAGACCAGGTGAACATTACAGAATTTTACACAGAGTCTCTCGTGCCTTCAAG 391

Qy        172 GAGAATAGAGGAGAACATCCAGTGTGGGGAGAACTTCATGGACAATAGAGTTTCATGGTC 231
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 GAGAATAGAGGAGAACATCCAGTGTGGGGAGAACTTCATGGACAATAGAGTTTCATGGTC 451

Qy        232 CTGAACCCCAGCCAGCAGCTGGCCATGTCGAGTCCCTGTTCCCTCACGCTGGGGCACCTTCACG 291
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        452 CTGAACCCCAGCCAGCAGCTGGCCATGTCGAGTCCCTGTTCCCTCACGCTGGGGCACCTTCACG 511

Qy        292 GTCCTGGAGAACCTCCTGTGTGCGTCATCCTCCAGCCTCCGCTGCAGG 351
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        512 GTCCTGGAGAACCTCCTGGTGCTGGGGTCATCCTCCAGCCTCCGCTGCAGG 571

Qy        352 CCTTCCTACCACTTCATCGGCAGCAGCCTGGCCCTCCACTCCCGGCGGAGTGTCTTCATTTTT 411
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        572 CCTTCCTACCACTTCATCGGCAGCAGCCTGGCCGTGGCACAGCCTCCACTCCCGGCGGAGTGTCATTTTT 631

Qy        412 GTCTACAAGCTTCATTGACTTCCACGTGGTTCCACGTGTTCCACGTGTTGCACATGGGGGAAG 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        632 GTCTACAGCTTCATTGACTTCCACGTGTTCACCGCAAAGATAGCCCGCAAACGTGTTTCTG 691

Qy        472 TTCAAACTGGGTGGGGTTCACGGGCCTCCTTCACTGCCTCCGTGGGCAGCCTGTTCCTCACA 531
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        692 TTCAAACTGGGTGGGGTTCACGGGCCTCCTTCACTGCCTCCGTGGGCAGCCTGTTCCTCACA 751

Qy        532 GCCATCGACAGGTACATATCCATTCACAGGCCCCTGGCCTATAAGAGAGGATTTGTCACCAGG 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        752 GCCATCGACAGGTACATATCCATTCACAGGCCCCTATAAGAGAGGATTTGTCACCAGG 811

Qy        592 CCCAAGGCCGTGTAGCCGTTTTTGCCCTGATGTGTGAGCCATTGGTGAAGTCGGCTGCTG 651
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        812 CCCAAGGCCGTGTAGCCGTTTTTGCCCTGATGTGTGACCATTGGTGATCGGCCGTGCTG 871

Qy        652 CCTCTCCTGGGCGTGGAACTGCGAGAAACTGCAATCGTGTTGCTCAGACATTTTCCCACAC 711
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        872 CCTCTCCTGGGGCGTGGAACTGCCGAGAAACTGCAATCTGTTTGCTTCAGACATTTTCCCACAC 931

Qy        712 ATTGATGAAAACCTACCTGATGTTGTGGGATCGGCGGCTCACCAGCGTGCTCCTTCGTTCATC 771
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        932 ATTGATGAAAACCTACCTGATGTTCTCGGATCGGCGGCTCACCAGCGTACTGCTTCGTTCATC 991

Qy        772 GTGTATGCGTACATGTATATTCTCTGGAAAGGCTCACAGCCACCAGCCGTCCGCATGATTCAG 831
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        992 GTGTATGCGTACATGTATATTTCTCTGGAAAGGCTCACAGCCACCAGCCGTCCGCATGATTCAG 1051

Qy        832 CCTGGCCACCCAGAAGAGCATCATCATCCACACGTCTCTGAGGATGGGGAAGGTACAGGTGACC 891
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1052 CCTGGCCACCCAGAAGAGACCATCATCATCCACACGTCTCTGAGGATGGGGAAGGTACAGGTGACC 1111

Qy        892 CGGCCAGACCAAGCCCGCCATGGACATTAGGTTAGCCAAGACCCTGGTCGTCCATCGATCCTGGTG 951
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1112 CGGCCAGACCAAGCCCGCCATGGACATTAGGTTAGCCAAGACCCTGGTCCTGGATCGATCCTGGTG 1171

Qy        952 GTGTTGATCATCTGCTGGGGCCCTCTGCTTCGAAATCATCAGGGTGTATGATTGTCTTTGGGAAG 1011
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1172 GTGTTGATCATCTGCTGGGGCCCCTCTGCTTGCAAATCATCAGGGTGTATGATGTCTTTGGGAAG 1231

Qy       1012 ATGAACAAGCTCATTAAGCACGGTGTTTGCATTCTGCACGTATGCTTCTGCCTGCTGAACTCC 1071
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1232 ATGAACAAGCTCATTAAGCACGGTGTTTGCATTCTGCACGTATGCTTCTGCCTGCTGAACTCC 1291

Qy       1072 ACCGTGAACCCATCATTCTATGCTTCTGAGGAGTAAGGACCTGGACAACACGCCTTTCCGGAGC 1131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1292 ACCGTGAACCCCATCATTCTATGCTTCTGAGGAGTAAGGACCTGGACACGCCTTTCCGGAGC 1351

Qy       1132 ATGTTTCCCTCTTGTGAAGGCACTGCGCAGCCTTCTGGATAACAAGACCATGGGACTCGGAC 1191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1352 ATGTTTCCCTCTTGTGAAGGCACTGCGCAGCCTTCTGGATAACAAGACCATGGGACTCGGAC 1411

Qy       1192 TGCCTGCACAAACACGGCAAAACAATGCAGCCAGTGTTCACAGGCCCGCAGAAAAGCTGCATC 1251
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1412 TGCCTGCACAAACACGGCAAAACAATGCAGCCAGTGTTCACAGGCCCGCAGAAAAGCTGCATC 1471

Qy       1252 AAGACACGGTCAAGATTGCCAAGGTAACCATGTCTCTGTGTGTCCACAGACAGCGTCTGCCGAG 1311
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1472 AAGACACGGTCAAGATTGCCAAGGTAACCATGTCTCTGTGTGTCCACAGACAGCGTCTGCCGAG 1531

Qy       1312 GCTCTGTGA 1320
              |||||||||
Db       1532 GCTCTGTGA 1540
```

RESULT 4
ACH91680
ID   ACH91680 standard; DNA; 1419 BP.
XX
AC   ACH91680;
XX
DT   29-JUL-2004 (first entry)
XX
DE   Human genome derived single exon probe #24875.
XX
KW   Human; probe; ss; gene expression; single exon probe; microarray;
KW   alternative splicing event; genomic alteration.
XX
OS   Homo sapiens.
XX
PN   US2003194704-A1.
XX
PD   16-OCT-2003.
XX
PF   03-APR-2002; 2002US-00029386.
PF
PR   03-APR-2002; 2002US-00029386.
XX
PA   (PENN/) PENN S G.
PA   (RANK/) RANK D R.
PA   (HANZ/) HANZEL D K.

```
XX
PT   Penn SG, Rank DR, Hanzel DK;
XX
DR   WPI; 2004-119264/12.
XX
PT   New human genome-derived single exon nucleic acid probes useful for human
PT   gene expression analysis, for identifying or characterizing alternative
PT   splicing events, for assessing genomic alterations or as tools for
PT   surveying tissues.
XX
PS   Claim 1; SEQ ID NO 24875; 80pp; English.

CC   The invention relates to a nucleic acid probe for measuring human gene
CC   expression, comprising any of the 27,400 fully defined nucleotide
CC   sequences in the specification, or their complements or fragments, and
CC   encoding at least 8 amino acids of any of the 6888 amino acid sequences
CC   fully defined in the specification. The probe is a single exon probe that
CC   hybridises under high stringency conditions to a nucleic acid molecule
CC   expressed in human cells or tissues. Also included are a spatially-
CC   addressable set of single exon nucleic acid probes for measuring human
CC   gene expression (comprising a plurality of single exon nucleic acid
CC   probes cited above, where each of the plurality of probes is separately
CC   and addressably isolatable or amplifiable from the plurality), a single
CC   exon microarray for measuring human gene expression, a method of
CC   measuring human gene expression, a vector comprising the single exon
CC   probe cited above, an ORF-encoded peptide comprising at least 8
CC   contiguous amino acids of any of the above-mentioned amino acid
CC   sequences (optionally with conservative amino acid substitution), an
CC   isolated antibody that binds specifically to a peptide cited above, and
CC   methods of selling and/or licensing single exon probes or microarrays to
CC   a customer desiring to measure gene expression, a method of providing
CC   human gene expression data by subscription, and a computer-readable
CC   storage medium which contains a database having a plurality of records
CC   (each record including data on the expression of a single exon probe
CC   cited above. The probe, methods and apparatus are useful in gene
CC   expression analysis. The probes may be used as tools for surveying
CC   tissues to detect the presence of expressed messages that contain their
CC   specific exon, or in constructing genome-derived single exon microarrays.
CC   In addition, the probes are used in identifying and characterising
CC   alternative splicing events, that includes their exon, in assessing
CC   smaller genomic alterations, in priming the synthesis of nucleic acids,
CC   or in expressing the ORF-encoded peptide. The present sequence is a human
CC   single exon probe of the invention. Note: The sequence data for this
CC   patent did not form part of the printed specification, but was obtained
CC   in electronic format directly from USPTO at
CC   seqdata.uspto.gov/sequence.html?DocID=20030194704
XX
SQ   Sequence 1419 BP; 321 A; 409 C; 355 G; 334 T; 0 U; 0 Other;

Query Match           95.3%;  Score 1257.8;  DB 12;  Length 1419;
Best Local Similarity  99.4%;  Pred. No. 0;
Matches 1262;  Conservative  0;  Mismatches  7;  Indels  0;  Gaps  0;

Qy          52 ACTGACCTCCTCCTGGGAAGTCCCTTCCAAGAGAAGAGATGACTGCGGGAGCAACCCCAGCTA 111
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         451 ACTTCCTTTAGGGGAGTCCCTTCCAAGAGAAGAGATGACTGCGGGAGCAACCCCAGCTA 510
```

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XX
AC   AAQ14003;
XX
DT   25-MAR-2003 (revised)
DT   17-DEC-2001 (revised)
DT   19-DEC-1991 (first entry)
XX
DE   Human cannabinoid receptor coding sequence.
XX
KW   Cannabis sativa; marijuana; drug test; substance K receptor; ss.
OS   Homo sapiens.
XX
PN   USN7564075-N.
XX
PR   08-AUG-1990;   90US-00564075.
XX
PF   08-AUG-1990;   90US-00564075.
XX
PD   03-SEP-1991.
XX
PA   (USSH )  NAT INST OF HEALTH.
PA   (USDC )  US SEC OF COMMERCE.
PI   Matsuda L, Brownstein M;
XX
DR   WPI; 1991-303326/41.
DR   P-PSDB; AAR14196.
XX
PT   DNA encoding mammalian cannabinoid receptor - used for producing receptor
PT   for screening mammalian cannabinoid receptor drugs and ligands and in detection.
XX
PS   Disclosure; Fig 5; 25pp; English.
XX
CC   SKR6 cDNA encoding the rat cannabinoid receptor was isolated from a rat
CC   cerebral cortex cDNA library. An EcoRI-XbaI fragment was used to screen a
CC   human cosmid library. A positive clone was identified and sequenced.
CC   There is ca. 97 per cent homology between the deduced amino acid
CC   sequences of the human and rat cannabinoid receptors. (N.B. the
CC   nucleotide sequence encoding the rat cannabinoid receptor is also given
CC   in the Specification but the copy quality is extremely poor; hence it is
CC   not included in N-Geneseq). Recombinantly produced receptor can be used
CC   to screen for new drugs suitable for treatment of cannabinoid-treatable
CC   conditions, e.g. glaucoma, bronchial asthma, etc. See also AAR14195.
CC   (Note: Revised entry submitted to correct the patent number format of US
CC   Government-owned NTIS applications to prevent clashes with ongoing US
CC   granted patent numbers. For further information please visit the Derwent
CC   web site at www.derwent.com/dwpi/updates/ntis_us.html.) (Updated on 25-
CC   MAR-2003 to correct PA field.)
XX
SQ   Sequence 1507 BP; 350 A; 428 C; 371 G; 358 T; 0 U; 0 Other;
```

```
FH   Key             Location/Qualifiers
FT   CDS             29..1447
FT                   /*tag= a
FT                   /product= "human cannabinoid receptor"
```

```
Query Match    95.3%;    Score 1257.8;    DB 2;    Length 1507;
Best Local Similarity   99.4%;    Pred. No. 0;    Mismatches 7;    Indels 0;    Gaps 0;
Matches 1262;    Conservative  0;    Mismatches  7;    Indels  0;    Gaps  0;
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```
Qy         52 ACTGACCTCCTCGGGAGCTCCCTTCCAAGAGGAAGAGATGACTCGGCCATTGCAGTGCCTCGTCCCTTCACG 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        179 ACTGACCTCCTCGGGAGCTCCCTTCCAAGAGGAAGAGATGACTCGGCCATTGCAGTGCCTCGTCCCTTCACG 238

Qy        112 GTCCCAGCAGACCAGGTGAACATTACAGAATTTACAACAAGTCTCTTCGGGGAGCAACCCCAGCTA 171
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 GTCCCAGCAGACCAGGTGAACATTACAGAATTTACAACAAGTCTCTTCGGGGAGCAACCCCAGCTA 298

Qy        172 GAGAATGAGGAGAGAAACATTCCAGTGTGGGGAGCAGTTGGGGAG 231
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        299 GAGAATGAGGAGAGAAACTTCATGGACATAGAGTGTTTCATGGTC 358

Qy        232 CTGGAACCCCAGCCAGCAGCAGCTGGCCATTGCAGTGCCTCGTCCCTTCACG 291
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        359 CTGGAACCCCAGCCAGCAGCAGCTGGCCATTGCAGTGCCTCGTCCCTTCACG 418

Qy        292 GTCCTGGAGAACCTCCTGGGTCGTGTGGCGTCCATCCTCACCACTCCCGGCTCAGG 351
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        419 GTCCTGGAGAACCTCCTGGGTCGTGTGGCGTCCATCCTCACCACTCCCGGCTCAGG 478

Qy        352 CCTTCCTACCACTTCATCGGCGACCTGGGGCGTGGCAGAGGATCATTTT 411
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db        479 CCTTCCTACCACTTCATCGGCGACCTGGGGCGTGGCAGAGGATCATTTT 538

Qy        412 GTCTACAGCTTCATTGACTTTGACTTGTTCCACCGCAAAGATAGCCCAAACGTGTTTCTG 471
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        539 GCCATCGACACAGGTTACATATTCCACGTGTTTCACCGCAAAGATAGCCCAAACGTGTTTCTG 598

Qy        472 TTCAAACTGGGTGGGGTCACGGCGGCTCCTTCACTCGGTGGGGCAGCTGTTCCTCACA 531
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        599 TTCAAACTGGGTGGGGTCACGGCGGCTCCTTCACTCGGTGGGGCAGCTGTTCCTCACA 658

Qy        532 GCCATCGACACAGGTTACATATCCATTCACAGGCCCTGGCCTATAAGGAGGATTGTCACCAGG 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        659 GCCATCGACACAGGTTACATATCCATTCACAGGCCCTGGCCTATAAGGAGGATTGTCACCAGG 718

Qy        592 CCCAAGGCCGTGGTAGCGTTTTGCCTGAGTGGACATAGCCATTGTGATCCGCGTGCTG 651
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 CCCAAGGCCGTGGTAGCGTTTTGCCTGAGTGGACATAGCCATTGTGATCCGCGTGCTG 778

Qy        652 CCTTCTCCTGGGTCTGGGACTGCCGAGAAACTGCAAATCTGTTTGCTCAGATCATTTTCCCACAC 711
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        779 CCTTCTCCTGGGTCTGGGACTGCCGAGAAACTGCAAATCTGTTTGCTCAGATCATTTTCCCACAC 838

Qy        712 ATTGATGAAAGCTTACCTGAGTTGTTCGGATCGGGGTCACCAGGGTACTTCATC 771
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        839 ATTGATGAAAGCTTACCTGAGTTGTTCGGATCGGGGTCACCAGGGTACTTCATC 898

Qy        772 GTGTATGGGGTACATGTATATTTCTCTGGAAAGGTCACAGCCACCGCCGGTCCGCATGATTCAG 831
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        899 GTGTATGGGGTACATGTATATTTCTCTGGAAAGGTCACAGCCACCGCCGGTCCGCATGATTCAG 958

Qy        832 CGTGGGCACCCAGAAGAGCAATCATCATCCACACGTCTCGAGGATGGGAAGGTACAGGTGACC 891
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        959 CGTGGGCACCCAGAAGAGCAATCATCATCCACACGTCTCGAGGATGGGAAGGTACAGGTGACC 1018

Qy        892 CGGCCAGACCAAGCCCGCATGGACATTAGGTTAGCCAAGACCCTGGTCCTGGTCGGTG 951
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1019 CGGCCAGACCAAGCCCGCATGGACATTAGGTTAGCCAAGACCCTGGTCCTGGTCGGTG 1078

Qy        952 GTGTTGATCCATCTGGGGCCCCTCTCGTTCTGCTTTGCAAATCATGGTTGTATGAGTGTTCTTTGGGAAG 1011
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1079 GTGTTGATCATCTGGGGCCCCTCTCGTTCTGCTTTGCAAATCATGGTTGTATGAGTGTTCTTTGGGAAG 1138

Qy       1012 ATGAACAAGCTCATTAAGCACGGTGTTTTGCATTCTGCAGTATGCTTCTGAACTCC 1071
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1139 ATGAACAAGCTCATTAAGCACGGTGTTTTGCATTCTGCAGTATGCTTCTGAACTCC 1198

Qy       1072 ACCGTGAACCCATCATCTATGCTTCTGAGGAGTAAGGACCTGGCACAGCTTTCCAGGAGC 1131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1199 ACCGTGAACCCATCATCTATGCTTCTGAGGAGTAAGGACCTGGCACAGCTTTCCAGGAGC 1258

Qy       1132 ATGTTTCCCTCTTGTGAAGGCACTGCGCAGCCTCTCGGATAACAGCATGGGGGACTCGGAC 1191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1259 ATGTTTCCCTCTTGTGAAGGCACTGCGCAGCCTCTCGGATAACAGCATGGGGGACTCGGAC 1318

Qy       1192 TGGCCTGCACAAACACGCAAAACAAATGCAGCCAGTGTTCACAGGGCCGCAGAAAAGCTGCATC 1251
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1319 TGGCCTGCACAAACACGCAAAACAAATGCAGCCAGTGTTCACAGGGCCGCAGAAAAGCTGCATC 1378

Qy       1252 AAGAGCACGGTCAAGAATGCCAAGGTAACCATAGTCTGTTGTGTCCACAGACAGCGTCTGCCAGG 1311
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1379 AAGAGCACGGTCAAGAATTGCCAAGGTAACCATGTCTGTTATCCACAGAGACACGTCTGCCAGG 1438

Qy       1312 GCTCTGTGA 1320
              |||||||||
Db       1439 GCTCTGTGA 1447
```

Db

RESULT 6
ID   ABZ42646 standard; DNA; 1755 BP.
XX
AC   ABZ42646;
XX
DT   04-MAR-2003 (first entry)
XX
DE   Human cannabinoid receptor 1 nucleotide SEQ ID NO:83.
XX
KW   G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW   G protein-coupled receptor modulator; antibody; immune-related disease;
KW   growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW   immunological-related cell proliferative disease; autoimmune disease;
KW   Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW   osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW   graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW   psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW   mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW   hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW   ulcer; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO20261087-A2.
XX
PD   08-AUG-2002.
XX
PF   19-DEC-2001; 2001WO-US050107.
XX
PR   19-DEC-2000; 2000US-0257144P.
XX
PA   (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI   Burmer GC, Roush CL, Brown JP;
XX
DR   WPI; 2003-046718/04.
DR   N-PSDB; ABP81800.
XX
PT   New isolated antigenic peptides e.g. for G protein-coupled receptors
PT   (GPCR), useful for diagnosing and designing drugs for treating conditions
PT   in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT   autoimmune diseases.
XX
PS   Disclosure; Fig 1; 523pp; English.
XX

The present invention describes antigenic peptides (I) comprising: (a)
any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
acids. Also described: (1) an assay for the detection of a particular G
protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
and (2) an isolated antibody having high specificity and high affinity or
avidity for a particular GPCR. (I) can be used as GPCR modulators and in
gene therapy. The antigenic peptides for GPCRs are useful in detecting an
antibody against a particular GPCR, and in the production of specific
antibodies. The peptides and antibodies are also useful for detecting the
presence or absence of corresponding GPCRs. The antigenic peptides for
GPCRs and antibodies are useful for diagnosing and designing drugs for
treating immune-related diseases, growth-related diseases, cell
regeneration-related disease, immunological-related cell proliferative
diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
atherosclerosis, bacterial, fungal, protozoan or viral infections,
osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
inflammation, allergies, Crohn's disease, diabetes, graft versus host
disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
anxiety, depression, schizophrenia, dementia, mental retardation, memory
loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
any other disorder in which GPCRs are involved. The antibodies may be
used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode

CC   GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC   exemplification of the present invention
XX
SQ   Sequence 1755 BP; 395 A; 487 C; 441 G; 432 T; 0 U; 0 Other;

Query Match   95.3%; Score 1257.8; DB 8; Length 1755;
Best Local Similarity   99.4%; Pred. No. 0;
Matches 1262; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```
Qy     52 ACTGAACCTCCTTGGGGAAGTCCCTTCCAAGAAGAAGGAAGGATGACTGGCGGAGGACAACCCCCAGCTA 111
          ||||||| ||||||||||||||||||||||||||||||    ||||||||||||||||||||||||||||
Db    299 ACTTCCTTTAGGGGAAGTCCCTTCCAAGAAGAAGAATGACTGGCGGAGGACAACCCCCAGCTA        358

Qy    112 GTCCCAGCAGGACCAGGTGAACATTACAGAATTTACAGAACAAAGTCTTCTCTCGGTCCTTCAAG       171
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    359 GTCCCAGCAGGACCAGGTGAACATTACAGAATTTTACAGACAAAGTCTCTCTCGGTCCTTCAAG        418

Qy    172 GAGAATGAGGAGAACATTCCAGTGTGGGGAGAACTTCATGGAGAAGTGTTTCATGGGTC             231
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    419 GAGAATGAGGAGAACATTCCAGTGTGTGGGAGAACTTCATGGACATAGAGTTTTCATGGGTC          478

Qy    232 CTGAACCCCAGCCAGCGCAGCGTGGCCATTGCAGTCTGTTCCCTCACGGTCGGCCACCTTCACG       291
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    479 CTGAACCCCAGCCAGCAGCGTGGCCATTGCAGTCTGTTCCCTCACGGTCGGCCACCTTCACG          538

Qy    292 GTCCTGGAGAAACCTCCTGGTGCGTGTGCGGTCATCCTCCACTGTCCCACTGTCATTGTT            351
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    539 GTCCTGGAGAAACCTCCTGGTGCGTGTGCGGTCATCCTCCACTGTCCCACTGTCATTGTT            598

Qy    352 CCTTCCTACCACTTCATCGGCGACCTGGCCGTGACCTCCTTGGGGAGTGGAGTTGTCATTGTTT        411
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    599 CCTTCCTACCACTTCATCGGCGACCTGGCCGTGACCTCCTTGGGGAGTGGAGTTGTCATTGTTT         658

Qy    412 GTCTTACAGCTTCATTGACTTCCACGTGTTCCACGCCAAAGATAGCGCAAGGTGTTTCTG            471
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    659 GTCTTACAGCTTCATTGACTTCCACGTGTTCCACGCCAAAGATAGCGCAAGGTGTTTCTG            718

Qy    472 TTCAAACTGGGTGGGGGTCACGGCCTTCCTTCACTCGTCGGTGGGCGAGCCTTGTTCCTCACA         531
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    719 TTCAAACTGGGTGGGGGTCACGGCCTTCCTTCACTCGTCGGTGGGCGAGCCTTGTTCCTCACA         778

Qy    532 GCCATCGACAGGTACATATCCATTCACAGGCCCCTGCCTATAAGAGGGATTGTCACCAGG           591
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    779 GCCATCGACAGGTACATATCCATTCACAGGCCCCTGGCCTATAAGAGGGATTGTCACCAGG           838

Qy    592 CCCAAGGCGCGTGGTAGCGTTTTGCCTGATGGTGGACCATAGCCATTGTGATCGGCTG             651
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    839 CCCAAGGCGCGTGGTAGCGTTTTGCCTGATGGTGGACCATAGCCATTGTGATCGGCTG             898

Qy    652 CCCTCTCCTGGGCTGGAACTGCGAGAAAACTGCAATCTGTTTGTCTCAGACACATTTCCCACAC       711
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    899 CCTCTCCTGGGCTGGAACTGCGAGAAAACTGCAATCTGTTTGTCTCAGACATTTCCCACAC          958

Qy    712 ATTGGATGAAAACTTACCTGATTCGTGGATCGGCGGGTCACCAGGGCTACTGGTTCGTTCATC         771
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    959 ATTGGATGAAAACTTACCTGATTGTCTGGATCGGGGGTCACCAGGGCTACTGTTTCGTTCATC         1018

Qy    772 GTGTATGCGTACATGTATATTCTTCTGGGAAGGTCCACAGCCACGCCGTCCGCATGGATTCAG        831
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1019 GTGTATGCGTACATGTATATTCTTCTGGGAAGGTCCACAGCCACGCCGTCCGCATGGATTCAG        1078

Qy    832 CGTGGCCACCCAGAAGAGCATCACATCCACACCTCTGAGGATGGGAAGGTACAGGTGACC          891
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1079 CGTGGCCACCCAGAAGAGCATCACATCCACACCTCTGAGGATGGGAAGGTACAGGTGACC          1138

Qy    892 CGGCCAGACCAAGCCCCGGCCATGACATTAGGTTAGCCAAGACCCTGGGTCCCTGGCTGCTG        951
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1139 CGGCCAGACCAAGCCCCGCATGGACATTAGGTTAGCCAAGACCCTGGGTCCTGACCCTGGCTG        1198

Qy    952 GTGTTGATCATCTGCTGGGGCCCCTGCTTGCAATCATGGTGTATGATGTCTTTGGGGAAG          1011
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1199 GTGTTGATCATCTGCTGGGGCCCCTGCTTGCAATCATGGTGTATGATGTCTTTGGGGAAG          1258
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Qy    1012 ATGAACAAGCTCATTAAGACACGGTGTTTGCATTCTGCAGTATGTCTCTGCCTGCTGAACTCC 1071
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1259 ATGAACAAGCTCATTAAGACGGTGTTTGCATTCTGCAGTATGTCTCTGCCTGCTGAACTCC 1318

Qy    1072 ACCGTGAAACCCCATCATCTATGCTTCGAGGAGTAAGGACCTTGCGACGCTTTCCGGAGC 1131
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1319 ACCGTGAAACCCCATCATCTATGCTCTGAGGAGTAAGGACCTTGCGACGCTTTCCGGAGC 1378

Qy    1132 ATGTTCCCTCTTGTGAAGGCACTGCCCAGCCTTCTGGATAACAGACATGGGGGGGGGGAC 1191
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1379 ATGTTTCCCTCTTGTGAAGGCACTGCCCAGCCTTCTGGATAACAGACATGGGGGGGGGGAC 1438

Qy    1192 TGCCTGCACAAAACACCGAAAACAAATGCAGCCAGTGTTCACAGGGCCCCAGAAAGCTCATC 1251
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1439 TGCCTGCACAAAACACCGAAAACAAATGCAGCCAGTGTTCACAGGGCCCGAGAAAGCTGCATC 1498

Qy    1252 AAGAGACACGGTGCAAGTTGCCAAGGTAACCATGTCTGTGTCCACAGACACGTTCTGCCGAG 1311
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1499 AAGAGACACGGTGCAAGATTGCCAAGGTAACCATGTCTGTGTCCACAGACACGTTCTGCCGAG 1558

Qy    1312 GCTCTGTGA 1320
                ||||||||
Db    1559 GCTCTGTGA 1567
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RESULT 7
ID       ADN38917 standard; cDNA; 1755 BP.
XX
AC       ADN38917;
XX
DT       17-JUN-2004 (first entry)
XX
DE       Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:235.
XX
OS       Homo sapiens.
PN       WO2003042661-A2.
XX
PD       22-MAY-2003.
XX
PF       13-NOV-2002; 2002WO-US036810.
XX
PR       13-NOV-2001; 2001US-0350666P.
PR       21-NOV-2001; 2001US-0332464P.
PR       29-NOV-2001; 2001US-0334393P.
PR       03-DEC-2001; 2001US-0335394P.
PR       14-DEC-2001; 2001US-0340376P.
PR       08-JAN-2002; 2002US-0347211P.
PR       10-JAN-2002; 2002US-0347349P.
PR       08-FEB-2002; 2002US-0355250P.
PR       13-FEB-2002; 2002US-0356714P.
PR       20-FEB-2002; 2002US-0359077P.
PR       29-MAR-2002; 2002US-0368809P.
PR       04-APR-2002; 2002US-0370110P.
PR       12-APR-2002; 2002US-0372246P.
PR       05-JUN-2002; 2002US-0386614P.
PR       16-JUL-2002; 2002US-0396839P.
PR       22-JUL-2002; 2002US-0397775P.
PR       22-JUL-2002; 2002US-0397845P.
PR       09-SEP-2002; 2002US-0409450P.
XX
PA       (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI       Afar D, Aziz N, Ginsburg WM, Gish KC, Glynne R, Hevezi PA;
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PI       Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX
DR       WPI; 2003-468649/44.
DR       P-PSDB; ADN38918.
XX
PT       Determining the presence or absence of a pathological cell in a patient,
PT       useful for diagnosing, prognosing or treating cancer, comprises detecting
PT       a nucleic acid in a biological sample.
XX
PS       Claim 8; SEQ ID NO 235; 1385pp; English.
XX
CC       The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC       whose expression is upregulated or downregulated in specific cancers or
CC       other diseases such as angiogenic or fibrotic disorders, and to methods
CC       of determining the presence or absence of a pathological cell in a
CC       patient by detecting a nucleic acid at least 80% identical to those of
CC       the invention or by detecting a polypeptide of the invention. The
CC       invention also relates to expression vectors and host cells comprising a
CC       nucleic acid of the invention; antibodies which specifically bind a
CC       polypeptide of the invention; use of such antibodies for drug targeting;
CC       and methods of screening for modulators of activity or expression of the
CC       polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC       antibodies and methods are useful for diagnosing, prognosing and treating
CC       cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC       atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC       neovascularisation syndromes, scarring and uterine fibroids. They may
CC       also be useful in wound healing and in contraception. The present
CC       sequence represents a nucleic acid sequence of the invention.
XX
SQ       Sequence 1755 BP; 395 A; 487 C; 441 G; 432 T; 0 U; 0 Other;

Query Match             95.3%;  Score 1257.8;  DB 11;  Length 1755;
Best Local Similarity   99.4%;  Pred. No. 0;
Matches 1262;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;
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```
Qy      52 ACTGACCTCCTGGGAAGTCCCTTCCAAGAGAGAGATGACTGCGGGAGACAACCCCAGCTA 111
                |||||   | |||||||||||||||||||||||||||||||||||||||||||||||||
Db     299 ACTTCCTTTAGGGGAAGTCCCTTCCAAGAGAAGATGACTGCGGGAGACAACCCCAGCTA 358

Qy     112 GTCCCAGCGAGACCAGGGTGAACATTACAGAANTTTTACAACAAGTCTCTCCGGCCTTCAAG 171
                |||||||||||||||||||||||||||||  |||||||||||||||||||||||||||
Db     359 GTCCCAGCAGACCAGGTGAACATTACAGANTTTACAACAAGTCTCTCTCGGCCTTCAAG 418

Qy     172 GAGAATGAGGAGAACATCCAGTGTGGGGAGGAGAACTTCATTGGACNATAGAGTGTTTCATTGGTC 231
                |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db     419 GAGAATGAGGAGAACATCCAGTGTGGGGAGGAGAACTTCATTGGACATAGAGTGTTTCATTGGTC 478

Qy     232 CTGAACCCCAGCCCAGCAGCTGGCCATTGCAGTCCGTGTCCCTGTCCTCACGGTTCGCACCTTCACG 291
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     479 CTGAACCCCAGCCCAGCAGCTGGCCATTGCAGTCCGTGTCCCTGTCCTCACGGTTCGCACCTTCACG 538

Qy     292 GTCCTGGAGAAACCTTCCTGTGCGTGCTGCCGTGCAGCCCTGGCAGCCTCCTGCCTGCAGG 351
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     539 GTCCTGGAGAAACCTTCCTGTGCGTGCTGCCGTGCAGCCCTGGCAGCCTCCTGCCTGCAGG 598

Qy     352 CCTTCCTTACCACTTCATCGGCGCAGCCTGCAGACCTTCCTTCTCCGGCGGAGTGTCATTTTT 411
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     599 CCTTCCTTACCACTTCATCGGCGCAGCCTGCAGACCTTCCTTCTCCGGCGGAGTGTCATTTTT 658

Qy     412 GTCTTACAGCTTCATTGACTTCCACGTGTTCCACGCCAAAGATAGCCGCCAACGTGTTTCTG 471
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     659 GTCTTACAGCTTCATTGACTTCCACGTGTTCCACGCAAAGATAGCCGCCAACGTGTTTCTG 718

Qy     472 TTCAAAACTGGGTGGGGGGTCACGGCCTCCTTCACTGCCTCCGTGGCGCAGCCTGTTCCTCACA 531
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     719 TTCAAAACTGGGTGGGGTCACGGCCTCCTTCACTGCCTCCGTGGCGCAGCCTGTTCCTCACA 778

Qy     532 GCCATCGACAGGGTACATATCCATTCACAGGCCCCTGCCTATAAGAGAGAGTTGTCACCAGG 591
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     779 GCCATCGACAGGGTACATATCCATTCACAGGCCCCTGCCTATAAGAGAGAGTTGTCACCAGG 838

Qy     592 CCCAAGGGCCGTGGTTAGCCGTTTGCCTGATGTGGACCATAGCCATTGTGATCGCCGTGCTG 651
                |||||||||||||||||||||||||||||||||
Db     779 GCCATCGACAGGGTACATATCCATTCACAGGCCCC 838
```

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XX
XX
PN   WO20040030615-A2.
XX
OS   Homo sapiens.
XX
KW   gene therapy; cytostatic; gene; 88.
KW   chromosome identification; chromosome mapping; gene mapping;
KW   cervical cancer; melanoma; leukaemia; hybridisation probe;
KW   central nervous system cancer; bladder cancer; pancreatic cancer;
KW   colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW   tumour; diagnosis; cell proliferative disorder; breast cancer;
DE   Tumour-associated antigenic target (TAT) cDNA DNA324834, SEQ ID NO:2079.
DT   18-NOV-2004 (first entry)
AC   ACN38515;
ID   ACN38515 standard; cDNA; 5471 BP.

RESULT 8
ACN38515
ACN38515
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Db   1559 GCTCTGTGA 1567
          |||||||||
Qy   1312 GCTCTGTGA 1320

Db   1499 AAGAGCACGGTCAAGATTGCCAAGGTAACCATGTCTGTGTCCAGAGACACGTCTGCGAG 1558
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1252 AAGAGCACGGTCAAGATTGCCAAGGTAACCATGTCTGTGTCCAGAGACACGTCTGCGAG 1311

Db   1439 TGCCTGCAAACACGCAAACAATGCACGCCAGTGTTCACGCGCCGCAGAAAAGCTGCATC 1498
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1192 TGCCTGCAAACACGCAAACAATGCACGCCAGTGTTCACGCGCCGCAGAAAAGCTGCATC 1251

Db   1379 ATGTTTCCCTCTTGTGAAGGCACTGCGCCCAGCGCCTCTGGATAACAGCATGGGGGGAC 1438
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1132 ATGTTTCCCTCTTGTGAAGGCACTGCGCCCAGCGCCTCTGGATAACAGCATGGGGGGAC 1191

Db   1319 ACCGTGAACCCCATCATCTATCGCTCTGAGGAGTAAGGACCTGGCACGCTTTCCGGAGC 1378
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1072 ACCGTGAACCCCATCATCTATCGCTCTGAGGAGTAAGGACCTGGCACGCTTTCCGGAGC 1131

Db   1259 ATGAACAAGCTCATTAAGACGGTGTTTGCATTCTGCAGTATGCTTCTGCCTGAACTCTC 1318
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1012 ATGAACAAGCTCATTAAGACGGTGTTTGCATTCTGCAGTATGCTTCTGCCTGAACTCTC 1071

Db   1199 GTGTTGATCATGTCTGCTTCGGGGTCCCTTCGCTTGCAATCATGGTGTATGATGCTTTGGGAAG 1258
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    952 GTGTTGATCATGTCTGCTTCGGGGTCCCTTCGCTTGCAATCATGGTGTATGATGCTTTGGGAAG 1011

Db   1139 CGGCCCAGACCAAGCCCCGCATGGACATTAGGGTTAGCCAAGGTTAGCAGCCGTCCTGATCCTGGTG 1198
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    892 CGGCCCAGACCAAGCCCCGCATGGACATTAGGGTTAGCCAAGGTTAGCAGCCGTCCTGATCCTGGTG 951

Db   1079 CGTGGGCACCCAGAAGAGCAATCATCATCCACACGTCTCGAGGATGGGAAGGTACAGGTGACC 1138
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    832 CGTGGGCACCCAGAAGAGCAATCATCATCCACACGTCTCGAGGATGGGAAGGTACAGGTGACC 891

Db   1019 GTGTATCGGTACATGTATATATTCTCTGAAGGGGCTCACAGCCACCAGCCCCATGATTCAG 1078
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    772 GTGTATCGGTACATGTATATATTCTCTGAAGGGGCTCACAGCCACCAGCCCCATGATTCAG 831

Db    959 ATTGATGAAAACCTACCTGATGTTCTGGATCGGGGGTCACCAGCGTACTGCTTCTTCTGTTCATC 1018
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    712 ATTGATGAAAACCTACCTGATGTTCTGGATCGGGGGTCACCAGCGTACTGCTTCTTCTGTTCATC 771

Db    899 CCTCTCCTGGGCTGGAACTGCGAAACTGCAATCGTTTGCTCAGACATTTCCCACAC 958
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    652 CCTCTCCTGGGCTGGAACTGCGAAACTGCAATCGTTTGCTCAGACATTTCCCACAC 711

Db    839 CCCAAGGCCGTGGTGGCCTTTTGCCTGATGTGGACCATAGCCATTGTGATCGCCGTGCTG 898
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PD   15-APR-2004.
XX
PF   29-SEP-2003; 2003WO-US028547.
XX
PR   02-OCT-2002; 2002US-0414971P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Wu TD, Zhang Z, Zhou Y;
XX
DR   WPI; 2004-347921/32.
XX
PT   New tumor-associated antigenic target polypeptides and nucleic acids,
PT   useful in preparing a medicament for treating or detecting a
PT   proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT   prostate cancer or tumor.
XX
PS   Claim 1; SEQ ID NO 2079; 7273pp; English.
XX
CC   The invention relates to human tumour-associated antigenic target (TAT)
CC   polypeptides, and their related nucleic acids. The TAT polypeptides are
CC   overexpressed in cancer tissues compared to normal tissues, and may thus
CC   serve as effective targets for the diagnosis and treatment of cancer in
CC   mammals. The invention also relates to nucleic acid and polypeptide
CC   sequences at least 80% identical to the TAT nucleic acids and
CC   polypeptides; expression vectors and host cells comprising a TAT nucleic
CC   acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC   molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC   TAT polypeptide; and methods for the treatment or
CC   diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC   antibodies, antagonists, binding molecules and compositions are useful
CC   for diagnosing or treating a cell proliferative disorder associated with
CC   increased TAT expression, particularly cancers such as breast cancer,
CC   colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC   cancer, pancreatic cancer, cervical cancer, cancers of the central
CC   nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC   used as hybridisation probes, in chromosome and gene mapping, in
CC   chromosome identification and in gene therapy. The present sequence
CC   represents a TAT nucleic acid of the invention
XX
SQ   Sequence 5471 BP; 1551 A; 1148 C; 1089 G; 1683 T; 0 U; 0 Other;
```

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Query Match      95.3%;  Score 1257.8;  DB 13;  Length 5471;
Best Local Similarity   99.4%;
Matches 1262;  Conservative   0;  Mismatches   7;  Indels   0;  Gaps   0;
```

```
Qy    52 ACTGACCTCCTGGGAAGTCCCTTCCAACGAAGAAGATGACTGCGGGAGACAACCCCAGCTA 111
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   214 ACTTCCTTTAGGGGAAGTCCCTTCCAACGAAGAAGATGACTGCGGGAGACAACCCCAGCTA 273

Qy   112 GTCCCAGCAGACCAGGTGAACATTACAGAATTTTACAACAAGTCTCTCCGTCCTTCAAG 171
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   274 GTCCCAGCAGACCAGGTGAACATTACAGAATTTTACAACAAGTCTCTCCGTCCTTCAAG 333

Qy   172 GAGAATGAGGAGAACATCCAGTGTGGGGAGAACTTCATGGACAATAGAGTGTTTCATGGTC 231
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   334 GAGAATGAGGAGAACATCCAGTGTGGGGAGAACTTCATGGACAATAGAGTGTTTCATGGTC 393

Qy   232 CTGAACCCCAGCCAGCCAGCTGGGCCATTGCAGTCGTCCTGTCCCTCACGGTCTGGGCACG 291
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   394 CTGAACCCCAGCCAGCCAGCTGGGCCATTGCAGTCGTCCTGTCCCTCACGGTCTGGGCACG 453

Qy   292 GTCCTGGAGAACCTCCTGGTGTCGTGGCTCATCCTCCACTCCGCAGCTTCGCTGCAGG 351
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   454 GTCCTGGAGAACCTCCTGGTGTCGTGGCTCATCCTCCACTCCGCAGCCTCCGCTGCAGG 513

Qy   352 CCTTCCTACCACTTCATCGGCAGCAGCCTGGCAGGAGTGTCAGAACCTCCTGGGGAGGTGTCATTTT 411
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   514 CCTTCCTACCACTTCATCGGCAGCAGCCTGGCAGGAGTGTCAGAACCTCCTGGGGAGGTGTCATTTT 573

Qy   412 GTCTACAGCTTCATTGACTTCCACGTGTTCCACCGCAAAGATAGCCGCAACGTGTTTCTG 471
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   574 GTCTACAGCTTCATTGACTTCCACGTGTTCCACCGCAAAGATAGCCGCAACGTGTTTCTG 633
```

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RESULT 9
AEA81160
ID   AEA81160 standard; DNA; 5480 BP.
XX
AC   AEA81160;
XX
DT   25-AUG-2005  (first entry)
XX
DE   Human cannabinoid receptor 1 (brain) variant 1 DNA.
XX
KW   screening; obesity; nutritional disorder; anorectic; ds; gene;
XX
KW   cannabinoid receptor 1.
XX
OS   Homo sapiens.
XX
PN   US2005136465-A1.
XX
PD   23-JUN-2005.
XX
PF   22-DEC-2004; 2004US-00019829.
XX
PR   22-DEC-2003; 2003EP-00104902.
XX
PA   (CLER/) CLERC R G.
PA   (DUCH/) DUCHATEAU-NGUYEN G.
PA   (GARD/) GARDES C.
PA   (MIZR/) MIZRAHI J.
PA   (OSTE/) OSTENSON C.
XX
PI   Clerc RG, Duchateau-Nguyen G, Gardes C, Mizrahi J, Ostenson C;
XX
DR   WPI; 2005-457507/46.
DR   N-PSDB; AEA81221.
XX
PT   Screening test compounds that reduce and/or prevent obesity involves
PT   contacting cell expressing gene from alpha-two-glycoprotein.
XX
PS   Claim 8; SEQ ID NO 27; 21pp; English.
XX
CC   The invention relates to a novel method for screening for test compounds
CC   that reduce and/or prevent obesity. The method comprises contacting a
CC   cell expressing a gene selected from SEQ ID NO. 1-12 or 25-85, with a
CC   compound. The method of the invention demonstrates anorectic and/or prevent
CC   obesity. The current sequence is that of the human cannabinoid receptor 1
CC   (brain) variant 1 DNA of the invention. The sequence listing for the
CC   specification can be located via the USPTO web-site.
XX
SQ   Sequence 5480 BP; 1148 C; 1089 G; 1683 T; 0 U; 0 Other;

Query Match           95.3%;  Score 1257.8;  DB 14;  Length 5480;
Best Local Similarity 99.4%;
Matches 1262;  Conservative   0;  Mismatches   7;  Indels   0;  Gaps   0;

Qy     52 ACTGAACCTCCTGGGAAGTCCCTTCCAAGAGAAGAATGACTGCGGGGAGCAACCCCCAGCTA    111
          |||    | ||||| ||||||||||| ||||||||||||||||||||||||||||||||||||
Db    214 ACTTCCTTTAGGGAGAGTCCCTTCCCAAGAGAAGAATGACTGCGGGGAGCAACCCCCAGCTA    273

Qy    112 GTCCCAGCGAGACCAGGTGAACATTACAGAATTTTACAACAAGTCTCTCTCGTCCTTCAAG    171
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    274 GTCCCAGCGAGACCAGGTGAACATTACAGAATTTTACAACAAGTCTCTCTCGTCCTTCAAG    333

Qy    172 GAGAATGAGGAGGAAACATCCAGTGTGGGGAGAGACTTCATGGACATAGAGTGTTTCATGGTC    231
          ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db    334 GAGAATGAGGAGGAACATCCAGTGTGGGGAGAGACTTCATGGACATAGAGTGTTTCATGGTC    393

Qy    232 CTGAACCCCAGCCAGCAGCTGGGCCATTGCAGTCCAGTCCTGTCCCTCACGCGTCTCCTTCACG    291
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    394 CTGAACCCCAGCCAGCAGCTGGGCCATTGCAGTCCAGTCCTGTCCCTCACGCGTCTCCTTCACG    453

Qy    292 GTCCTGGAGAACCTCCTGTGCGTGCGGTCATCCTCCACTCCACTCCGCCAGCCTCCGCTGCAGG    351
          |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    454 GTCCTGGAGAACCTCCTGGTCATGCGGTCATCCTCCACTCCACTCCGCCAGCCTCCGCTGCAGG    513

Qy    352 CCTTCCTTACCACTTCATCGGCGCAGCCCTGCCGGTGGCGGTGGCCAGACCTCTGGGGTGCATTTTT    411
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    514 CCTTCCTTACCACTTCATCGGCGCAGCCCTGCCGGTGGCGGTGGCCAGACCTCTGGGGTGCATTTTT    573

Qy    412 GTCTACAGCTTCATTGACTTCCACGTGTTCCACCGCAAAGATAGCCGCGAACGTGTTTCTG    471
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db    574 GTCTACAGCTTCATTGACTTCCACGTGTTCCACCGCAAAGATAGCCGCGAACGTGTTTCTG    633

Qy    472 TTCAAACTGGGTGGGGTCACGGCGCTCCTTCACTGCCTGTTCCTCACA    531
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    634 TTCAAACTGGGTGGGGTCACGGCGCTCCTTCACTGCCTGTTCCTCACA    693

Qy    532 GCCATCGACACAGGTACATATCATTCACAGCGCCCCTGCCCTTCCGTGG    591
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db    694 GCCATCGACACAGGTACATATCATTCACAGCGCCCCTGCCCTTCCGTGG    753

Qy    592 CCCAAGGCCGTGGGGTAGCGTTTTGCCTGATGTGGGACCATAGCATTGTGATCGCCGGCCTGCTG    651
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    754 CCCAAGGCCGTGGGGTAGCGTTTTGCCTGATGTGGGACCATAGCATTGTGATCGCCGGCCTGCTG    813

Qy    652 CCTCTCCTGGGGCTGGGAACTGCGGAGAAACTGCAATCTGTTTGGCTTCAGACATTTCCCACAC    711
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    814 CCTCTCCTGGGGCTGGGAACTGCGGAGAAACTGCAATCTGTTTGGCTTCAGACATTTCCCACAC    873

Qy    712 ATTGATGAAACCTTACCTGATGGTTCTGGATCGGAGTCGGGGGTACCGTACTGGCTTCTTCATC    771
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    874 ATTGATGAAACCTTACCTGATGGTTCTGGATCGGAGTCGGGGGTACCGTACTGGCTTCTTCATC    933

Qy    772 GTGTATTGCGGTACATGTATATTCTTCTGGAAGGCTCACAGCCACCAGGTACTGGTTCCGCATGATTCAG    831
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    934 GTGTATTGCGGTACATGTATATTCTTCTGGAAGGCTCACAGCCACCAGGTACTGGTTCCGCATGATTCAG    993

Qy    832 CGTGGGCACCCAGAGAGACGCATCATCAATCCACACGGTCTCGAGGATGGGAAGGTACAGGTGACC    891
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    994 CGTGGGCACCCAGAGAGACGCATCATCAATCCACACGGTCTCGAGGATGGGAAGGTACAGGTGACC    1053

Qy    892 CGGCCAGCACCAAGCCCGCCATGGACATTAGGTTAGCCAAGACCCTGGTCTTCCTGATCCTGGTG    951
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1054 CGGCCAGCACCAAGCCCGCCATGGACATTAGGTTAGCCAAGACCCTGGTCTTCCTGATCCTGGTG    1113

Qy    952 GTGTTGATCATCTGCTGGGGCCCTCTCCTTGCAATCATGGGTGTATGAGTGTTCTTTGGGAAG    1011
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1114 GTGTTGATCATCTGCTGGGGCCCTCTCCTTGCAATCATGGGTGTATGAGTGTTCTTTGGGAAG    1173

Qy   1012 ATGAACAAGCTCATTAAGACGGTGTTTGCATTCTGCAGTATGCTCTGCCTGCTGAACTCC    1071
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1174 ATGAACAAGCTCATTAAGACGGTGTTTGCATTCTGCAGTATGCTCTGCCTGCTGAACTCC    1233

Qy   1072 ACCGTGAACCCCATCATCTATGCTCTGAGGAGTAAAGACCTGCGACACGGCTTTCCGGAGC    1131
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1234 ACCGTGAACCCCATCATCTATGCTCTGAGGAGTAAAGACCTGCGACACGGCTTTCCGGAGC    1293

Qy   1132 ATGTTTCCCTCTTGTGTGAAGGCACTGCGCGCAGCCCTCTGGATAAACAGCATGCCCGGAC    1191
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1294 ATGTTTCCCTCTTGTGTGAAGGCACTGCGCGCAGCCCTCTGGATAAACAGCATGCCCGGAC    1353

Qy   1192 TGCCCTGGACAAAAACAACGGCAAACAAATGCAGCAGTTCACAGGGCCCGAGAAAAGCTGCATC    1251
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1354 TGCCCTGGACAAAAACAACGGCAAACAAATGCAGCAGTTCACAGGGCCCGAGAAAAGCTGCATC    1413

Qy   1252 AAGAGCACGGTCAAGATTGCCAAGGTAACCAGTCTCTGTGTTCACAGCACGGTCGTGCCGAG    1311
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1414 AAGAGCACGGTCAAGATTGCCAAGGTAACCAGTCTCTGTGTTCACAGCACGGTCGTGCCGAG    1473

Qy   1312 GCTCTCTGTGA    1320
          |||||||||||
Db   1474 GCTCTCTGTGA    1482
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RESULT 10

ID   ADA24536 standard; cDNA; 5653 BP.
XX
AC   ADA24536;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human cDNA differential expressed in adipose tissue, INCYTE1383759.1.
XX
KW   88; differential expression; adipose tissue; cytostatic; hypotensive;
KW   antiarteriosclerotic; antidiabetic; anorectic; gene therapy;
KW   peroxisome proliferator-activated receptor gamma; PPARgamma;
KW   diabetes mellitus; obesity; hypertension; atherosclerosis; breast cancer;
KW   prostate cancer; colon cancer; polycystic ovarian syndrome.
XX
OS   Homo sapiens.
XX
FN   US200306272-A1.
XX
PD   22-MAY-2003.
XX
PF   29-JUL-2002; 2002US-00208408.
XX
PR   30-JUL-2001; 2001US-0308868P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Schebye XM;
XX
DR   WPI; 2003-606416/57.
XX
PT   New combination comprising several cDNAs, useful for preparing a
PT   composition for diagnosing or treating diabetes mellitus, obesity,
PT   hypertension, atherosclerosis, or cancer of the breast, prostate or
PT   colon.
XX
PS   Claim 1; Page 75-77; 84pp; English.
XX
CC   Then invention relates to a new combination comprising 55 cDNAs (ADA24485
CC   -ADA24539)or their complements that are differentially regulated in an
CC   adipose sample. Also included are detecting differential expression of
CC   one or more cDNAs in a sample containing nucleic acids, screening several
CC   molecules or compounds to identify a ligand that specifically binds a
CC   cDNA, a vector comprising the cDNA, a host cell containing the vector,
CC   producing a protein, screening several molecules or compounds, producing
CC   an antibody and the isolated antibody. The cDNAs comprise sequences which
CC   are upregulated or downregulated in response to peroxisome proliferator-
CC   activated receptor gamma (PPARgamma) agonist. The combination comprising
CC   several cDNAs is useful for preparing a composition for diagnosing or
CC   treating diabetes mellitus, obesity, hypertension, atherosclerosis,
CC   cancer of the breast, prostate or colon, or polycystic ovarian syndrome.
XX
SQ   Sequence 5653 BP; 1601 A; 1185 C; 1117 G; 1750 T; 0 U; 0 Other;

Query Match             95.3%;  Score 1257.8;  DB 9;  Length 5653;
Best Local Similarity   99.4%;
Matches 1262;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy    52 ACTGACCTCCTGGGAGAGTCCCTTCCAAGAGAAGAGATGACTGCGGGAGACAACCCCAGCTA 111
         |||                     ||||||||||||||||||||||||||||||||||||||
Db   260 ACTTCCTTTAGGGGAGGTCCCTTCCAAGAGAAGAGATGACTGCGGGAGACAACCCCAGCTA 319

Qy   112 GTCCCAGCAGCAGCCAGTGAACATTACAGAATTTACAACAAGTCGTCTCTCGTCCTTCAAG 171
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   320 GTCCCAGCAGCAGCCAGTGAACATTACAGAATTTACAACAAGTCGTCTCTCGTCCTTCAAG 379

Qy   172 GAGAATGAGGAGGAACATCCAGTGTGGGGAGGAGAACTTCATGGACATAGAGTGTTTCATGGTC 231
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   380 GAGAATGAGGAGGAACATCCAGTGTGGGGAGGAGAACTTCATGGACATAGAGTGTTTCATGGTC 439

Qy   232 CTGAACCCCAGCCAGCAGCTGGCCCATTGCAGTCCGTCCCTCACGGCTGGGCACCTTCACG 291
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   440 CTGAACCCCAGCCAGCAGCTGGCCCATTGCAGTCCGTCCCTCACGGCTGGGCACCTTCACG 499

Qy   292 GTCCTGGAGAACCTCCTGGTGCTGTGGGTCATCCTCCACTCCCGGCAGCCTCCCGTGCAGG 351
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   500 GTCCTGGAGAACCTCCTGGTGCTGTGGGTCATCCTCCACTCCCGGCAGCCTCCCGTGCAGG 559

Qy   352 CCTTCCTACCACTTCATCGGCAGCCTGCCGTGGTCGGCGGTGGCAGACCTCCTTGGGGAGTTGCAT 411
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   560 CCTTCCTACCACTTCATCGGCAGCCTGCCGTGGTCGGCGGTGGCAGACCTCCTTGGGGAGTTGCAT 619

Qy   412 GTCTACAGCTTCATTGACTTCCACGTGTTCCACGCGCAAAGATAGCCCGCAAGGTGTTCTG 471
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   620 GTCTACAGCTTCATTGACTTCCACGTGTTCCACGCGCAAAGATAGCCCGCAAGGTGTTTCTG 679

Qy   532 GCCATCGACAGCAGGTAGCATATCCATTCACAGGCCCTGGGCTTATAAGAGAGATTGTCACCAGG 591
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   634 TTCAAACTCGGGTGGGGGTCACGGCCTCCTTCACGTGCGTGGGGTCAGCGCCTCGTTCCTCACA 693

Qy   592 CCCAAGGCCGTGGTGTAGCGTGTTTGCCTGCCATAGCCATTGTGATCGCCGGTGCTG 651
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   694 GCCATCGACAGCAGGTACATATTCCATTCACAGAGGCCCTATAAGAGGATTGTCACCAGG 753

Qy   652 CCTCTCCTGGGCCTGGGAACTGCAGAGAAACTGCAATCGTGTTTGCTCAGACATTTTCCCACAC 711
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   754 CCCAAGGCCGTGGTGGGCGTTTTTGCCTGATGTGGACCATAGCCATTGTGATCGCCGGTGCTG 813

Qy   712 ATTGATGAAACCTTACCTGAGTTCTGGATTCGGGGGTCACCAGCCGTACTCGTCCTTCTCGTTCATC 771
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   814 CCTCTCCTGGGCTGGGGACTGCCGGATAAGTCTGTTTGCTCAGACATTTTCCCACAC 873

Qy   772 GTTGTATCGTACATGTATATTCTCTCGAAGGTCACAGCCGATCGCCAGGTCCGCATGAGATTCAG 831
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   874 ATTGATGAAACCTTACCTGATTCGGGGGGTCACCAGCCGTACTCGTCCTTCTCGTTCATC 933

Qy   832 CGTGGCACCCAGAAGAGCCATCATCCACACGTCTCAGGATGGGAGGAGGTACAGGTGACC 891
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   934 GTTGTATCGTACATGTATATTCTCTGGAAGGTCACAGCCACCCGGTCGCCATGGATCAG 993

Qy   892 CGGCCAGACCAAGCCCGCATGGACATTAGGTTAGCCAAGAGACCCTGGTCTTGATCCTGGTG 951
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   994 CGTGGCACCCAGAAGAGCCATCATCCACACGTCTCAGGATGGGAGGAGGTACAGGTGACC 1053

Qy   952 GTTGTTGATCATCGTGCTGCTGGGGGCCCTCGCCTTGCAATCATGGGTGTATGATGTCTTTGGGAAG 1011
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1054 CGGCCAGACCAAGCCCGCATGGACATTAGGTTAGCCAAGAACCCGGTCGCCATGGATCCTGGTG 1113

Qy  1012 ATGAACAAGCTCATTAAGACGGGTGTTGGCATTCTCGAGTATGCCTGCCTGCTGAACTCC 1071
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1114 GTGTTGGATCATCGTTGCATCATGGGTGTATGATGTCTTCTTTGGGAAG 1173

Qy  1072 ACCGTGAACCCCATCATCTATGCTGTCTGAGGAGTAAGAGACACCTCGACACGGCTTTCCGGAGC 1131
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1174 ATGAACAAGCTCATTAAGACGGTGTTTGCATTCTCGAGTATGCCTGCCTGCTGAACTCC 1233

Qy  1132 ATGTTTCCCTCTTGTGAAGGCACTGCGCCAGCCTTCTGGATAACAGCATGCGGGCGGACTCGGAC 1191
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1294 ATGTTTCCCTCTTGTGAAGGCACTGCGCCAGCCTTCTGGATAACAGCATGGGGGGGACTCGGAC 1353

Qy  1192 TGCCTGCAAAACACGGAAACAATGCAGCCAGTGTTCACAGGGCCGCAGAAAAGCTGCATC 1251
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1354 TGCCTGCAAAACACCGGAAACAATGCAGCCAGTGTTCACAGGGCCGCAGAAAAGCTGCATC 1413

Qy  1252 AAGAGCACGGTCAAGATTGCCAAAGGTAAACCATGTCTGTCTGTTCACAGGGCACGTCTGCCGAG 1311
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1414 AAGAGCACGGTCAAGATTGCCAAAGGTAACCATGTCTGTCTGTTCACAGACACGTCTGCCGAG 1473

Qy  1312 GCTCTGTGA 1320
         |||||||||
Db  1474 GCTCTGTGA 1482
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RESULT 11
ADH77049
ID   ADH77049 standard; DNA; 1419 BP.
XX
AC   ADH77049;
XX
DT   22-APR-2004  (first entry)
XX
DE   hCB-1 double constitutive mutant encoding DNA, SEQ ID 2.
XX
KW   Anorectic; neuroprotective; cardiovascular; respiratory;
KW   gastrointestinal; cannabinoid; CB; receptor; obesity; psychiatric;
KW   neurological; immune; cardiovascular; reproductive; endocrine; disorder;
KW   respiratory; immune; cardiovascular; reproductive; gastrointestinal; hCB-1 D213A; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2004008150-A1.
XX
PD   22-JAN-2004.
XX
PF   14-JUL-2003; 2003WO-GB003066.
XX
PR   17-JUL-2002; 2002SB-00002242.
XX
PA   (ASTR ) ASTRAZENECA AB.
PA   (ASTR ) ASTRAZENECA UK LTD.
XX
PI   Greasley P;
XX
DR   WPI; 2004-143121/14.
XX
PS   Claim 24; SEQ ID NO 2; 31pp; English.
XX
CC   The invention relates to a method for identifying an inverse agonist of a
CC   cannabinoid (CB) receptor comprising contacting a CB receptor test
CC   inhibitory agent with the cell expressing the constitutively active CB
CC   receptor. The method is useful in identifying an inverse agonist of a CB
CC   receptor. The true antagonist or inverse agonist is useful in preparing a
CC   medicament for treating a disorder associated with a CB
CC   receptor. The disorder is obesity, psychiatric and neurological
CC   disorders. They are also useful in treating immune cardiovascular,
CC   reproductive and endocrine disorders and also diseases related to
CC   respiratory and gastrointestinal systems. The current sequence represents
CC   the hCB-1 double constitutive mutant encoding DNA.
XX
SQ   Sequence 1419 BP; 320 A; 410 C; 355 G; 334 T; 0 U; 0 Other;

Query Match             95.2%;  Score 1256.2;  DB 12;  Length 1419;
Best Local Similarity   99.4%;
Matches 1261;  Conservative   0;  Mismatches   8;  Indels   0;  Gaps   0;
```

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RESULT 12
ADH77050

ID   ADH77050 standard; DNA; 1419 BP.
XX
AC   ADH77050;
XX
DT   22-APR-2004  (first entry)
XX
DE   hCB-1-D213A constitutive mutant encoding DNA, SEQ ID 3.
XX
KW   Anorectic; neuroprotective; cardiovascular; respiratory;
KW   gastrointestinal; cannabinoid; CB; receptor; obesity; psychiatric;
KW   neurological; immune; cardiovascular; reproductive; endocrine; disorder;
KW   respiratory; gastrointestinal; hCB-1 D213A; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2004008150-A1.
XX
PD   22-JAN-2004.
XX
PF   14-JUL-2003; 2003WO-GB003066.
XX
PR   17-JUL-2002; 2002SE-0002242.
XX
PA   (ASTR ) ASTRAZENECA AB.
PA   (ASTR ) ASTRAZENECA UK LTD.
XX
PI   Greasley P;
XX
DR   WPI; 2004-143121/14.
XX
PT   Identifying an inverse agonist of a cannabinoid (CB) receptor, useful in
PT   treating obesity, psychiatric and neurological disorders, comprises
PT   contacting a test inhibitory agent with constitutively active CB
PT   receptor.
XX
PS   Claim 24; SEQ ID NO 3; 31pp; English.
XX
CC   The invention relates to a method for identifying an inverse agonist of a
CC   cannabinoid (CB) receptor comprising contacting a CB receptor test
CC   inhibitory agent with the cell expressing the constitutively active CB
CC   receptor. The method is useful in identifying an inverse agonist of a CB
CC   receptor. The true antagonist or inverse agonist is useful in preparing a
CC   medicament for treating or preventing a disorder associated with a CB
CC   receptor. The disorder is obesity, psychiatric and neurological
CC   disorders. They are also useful in treating immune cardiovascular,
CC   reproductive and endocrine disorders and also diseases related to
CC   respiratory and gastrointestinal systems. The current sequence represents
CC   the hCB-1-D213A constitutive mutant encoding DNA.
XX
SQ   Sequence 1419 BP; 320 A; 410 C; 355 G; 334 T; 0 U; 0 Other;

Query Match     95.2%;   Score 1256.2;   DB 12;   Length 1419;
Best Local Similarity   99.4%;   Pred. No. 0;   Mismatches  8;
Matches 1261;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     52 ACTGAACCTCCTGGGAAGTCCCTTCCAAGAAGAGAAGTGACTGGCGGGGAGAAACCCCAGCTA 111
          ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db    151 ACTTCCTTTAGGGGAAGTCCCTTCCAAGAAGAAGTGACTGGCGGGGAGACAACCCCAGCTA 210

Qy    112 GTCCCAGCAGACCAGGTGAACATTACAGAATTTTACAACAAGTCTCTCGTCCTTCAAG 171
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    211 GTCCCAGCAGACCAGGTGAACATTACAGAATTTTACAACAAGTCTCTCGTCCTTCAAG 270

Qy    172 GAGAATGAGGAGAGAACATCCAGTGTGGGGAGAACTTCATGGACATAGAGTGTTTCATGGTC 231
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    271 GAGAATGAGGAGAGAACATCCAGTGTGGGGAGAACTTCATGGACATAGAGTGTTTCATGGTC 330

Qy    232 CTGAACCCCAGCAGCAGCTGGCCATTGCAGTCCTTCGTCCCTCACGCTGCGGGCACCTTCACG 291
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    331 CTGAACCCCAGCAGCAGCTGGCCATTGCAGTCCTTCGTCCCTCACGCTGCGGGCACCTTCACG 390

Qy    292 GTCCTGGAGAACCTCCTGGTGCTGGGCGTGTCATCCTCCACTCCCGCAGCCTTCCGCTGCAGG 351
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    391 GTCCTGGAGAACCTCCTGGTGCTGGGCGTGTCATCCTCCACTCCCGCAGCCTTCCGCTGCAGG 450

Qy    352 CCTTCCTACCACTTCATCGGCAGCCTGGCGGTGGCAGACCTCCTGGGGAGTGTCATTTTT 411
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    451 CCTTCCTACCACTTCATCGGCAGCCTGGCGGTGGCAGACCTCCTGGGGAGTGTCATTTTT 510

Qy    412 GTCTACAGCTTCATTGACTTCCACGTGTTCCACCGCAAAGATAGCCCGAACCGTGTTTCTG 471
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy    472 TTCAAACTGGGTGGGGTCACGGCGCTTCCTTCACTGCCTGCCTCCGTGGGGCCAGCGCTTCACA 531
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    571 TTCAAACTGGGTGGGGTCACGGCCTTCCTTCACTGCCTCCGTGGGGCCAGCGCTTCACA 630

Qy    532 GCCATCGACAGGTACATATCCATTCACAGGCCCCTGGCCTTATAAGAGAGGATTGTCACCAGG 591
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    631 GCCATCGCCAGGTACATATCCATTCACAGGCCCCTGGCCTTATAAGAGAGGATTGTCACCAGG 690

Qy    592 CCCAAGGGCCGTGTTAGCCTGTTTTGCCTGATGTGGACCATAGCCATTGTGATCGGCGTGCTG 651
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    691 CCCAAGGGCCGTGTTAGCCTGTTTTGCCTGATGTGGACCATAGCCATTGTGATCGGCGTGCTG 750

Qy    652 CCTCTCCTGGGCTGGAACTGCAAGAAACTGCAATCTGTTGTTTGCTCAGACATTTCCCACAC 711
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    751 CCTCTCCTGGGCTGGAACTGCGAGAAACTGCAATCTGTTGTTTGCTCAGACATTTCCCACAC 810

Qy    712 ATGATGAAACCTACCTGATTGTTCTGGATCGGGGGTCACCAGGCGTACTGCTTCTGTTCATC 771
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    811 ATGATGAAACCTACCTGATTGTTCTGGATCGGGGGTCACCAGGCGTACTGCTTCTGTTCATC 870

Qy    772 GTGTATGGGTACATGTATATTCTCTGGAAGGCTCACAGCCACACCGTCCGCATGATTCAG 831
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    871 GTGTATGGGTACATGTATATTCTCTGGAAGGCTCACAGCCACACCGTCCGCATGATTCAG 930

Qy    832 CGTGGGCACCCAGGAGAAGAGCATCATCATCCACACGTCTGAGGAGGTACAGGTGACC 891
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    931 CGTGGGCACCCAGGAGAAGAGCATCATCATCCACACGTCTGAGGAGGTACAGGTGACC 990

Qy    892 CGGCCAGACCAAGCCCGCATGGACATTAGGTTAGCCAAGACCCTGGTCCTTGATCCTGGTG 951
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    991 CGGCCAGACCAAGCCCGCATGGACATTAGGTTAGCCAAGACCCTGGTCCTTGATCCTGGTG 1050

Qy    952 GTGTTGATCATCTGCTGGGGCCCCCTTCTGCTTCGCCAATCATCATTGGGTGTAATGGTGTGGGAAG 1011
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1051 GTGTTGATCATCTGCTGGGGCCCCTTCTGCTTCGCAATCATGGTGTATGGGTGTCTTTGGGAAG 1110

Qy   1012 ATGAACAAGCTCATTAAGACGGTGTTTGCCATTCGCAGTGTATGGTCTTGCTGAACTCC 1071
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1111 ATGAACAAGCTCATTAAGACGGTGTTTGCATTCTGCAGTGTATGGTCTTGCTGAACTCC 1170

Qy   1072 ACCGTGAACCCCATCATCTATGCTCTGAGGAGTAAGGACCTGCGACACCTTTCCGGAGC 1131
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1171 ACCGTGAACCCCATCATCTATGCTCTGAGGAGTAAGGACCTGCGACACCTTTCCGGAGC 1230

Qy   1132 ATGTTTCCCTCTTGTGAAGGCACTGCGCAGCCTCTGGATAACAGCAGCAGCCTTCCGGAC 1191
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1231 ATGTTTCCCTCTTGTGAAGGCACTGCGCAGCCTCTGGATAACAGCAGCAGCCTTCCGGAC 1290

Qy   1192 TGCCTGCACAAACACGCAAACAATGCAGCCCAGTGTTCACAGGGGCCGCAGAAAAGCTGCATC 1251
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1291 TGCCTGCACAAACACGCAAACAATGCAGCCCAGTGTTCACAGGGGCCGCAGAAAAGCTGCATC 1350

Qy   1252 AAGAGCACGGTCAAGATTGCCAAGGTAACCAAGTCTCGTGTCAGACACACGTCTGCGAG 1311
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1351 AAGAGCACGGTCAAGATTGCCAAGGTAACCATGTCTCGTGTCAGACACACGTCTGCGAG 1410

Qy   1312 GCTCTCTGTGA 1320
          |||||||||||
Db   1411 GCTCTCTGTGA 1419
```

```
RESULT 13
AD029849
ID   AD029849 standard; cDNA; 1419 BP.
XX
AC   AD029849;
XX
DT   29-JUL-2004  (first entry)
XX
DE   Human GPCR CNR1 polynucleotide, SEQ ID NO:951.
XX

Db   511 GTCTACAGCTTCATTGACTTCACGTGTTCCACGGCGAAAGATAGCCCAACCTGTGTTCTG 570
Qy   472 TTCAAACTGGGGTGGGGTCACGGCGTCCTCCTTCACTGCGCTCCGTGGCGGGCAGCCGTG 531
             |||||||||||||||||||||||||||||||||||||||||||||||||
Db   571 TTCAAACTGGGGTGGGGTCACGGCGTCACGGCCTCCGTGGCGGGCAGCCGTGTTCCTCACA 630

Qy   532 GCCATCGACAGGTACATATCAATTCACAGGCCCCTGCCTATAAGAGAGGATTGTCACCAGG 591
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   631 GCCATCGACAGGTACATATCAATTCACAGGCCCCTGCCTATAAGAGAGGATTGTCACCAGG 690

Qy   592 CCCAAGCCGTGGTAGCCGTTTTTGCCTGATTGGAGCATAGCCATTGTGATCCCGGTGCTG 651
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   691 CCCAAGCCGTGGTGGGGTTTTGCCTGATTGGGACCATAGCCATTGTGATCCCGGTGCTG 750

Qy   652 CCTCTCCTGGGGGCTGGGAACTGCGAGAAACTGCAATCTGTTTGCTCAGACACATTTTCCCACAC 711
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   751 CCTCTCCTGGGGGCTGGGAACTGCGAGAAACTGCAATCTGTTTGCTCAGACACATTTTCCCACAC 810

Qy   712 ATTGATGAAAAACCTACCTGATGTTCTGATCGGGGTCACCGGGTACTGCGTTCTTCGTTCATC 771
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   811 ATTGATGAAAACCTACCTGATGTTCTGGATCGGGGTCACCGGGTACTGCTTCTGTTCATC 870

Qy   772 GTGTATGCGGTACATGTATATTCTTCTGGAAGGGCTTCACAGCCGTCCAGCCGCATGATTCAG 831
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   871 GTGTATGCGGTACATGTATATTCTCTGGAAGGGCTTCACAGCCGTCCAGCCGCATGATTCAG 930

Qy   832 CGTGGCACCCAGAGAGAGCATCATCATCCACAGCCTCTGAGGATGGGAAGGTACAGGTGACC 891
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   931 CGTGGCACCCAGAAGAGACATCATCCACAGCCTCTGAGGATGGGAAGGTACAGGTGACC 990

Qy   892 CGGCCAGACCAAGCCCGCATGGACATTAGGTTAGCCAAGACCCTGGTTCCTGATCCTGGTG 951
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   991 CGGCCAGACCAAGCCCGCATGGCCAATAGGGTGTTCCTGAAGAACCCCGGTCCTGGGTG 1050

Qy   952 GTGTTGATCATTCTGCTGGGCCCTCTTCGTTGCTCAATCATTGGTGTATGAGTGTCTTTGGGAAG 1011
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1051 GTGTTGATCATTCTGCTGGGCCCTCTTCGTTGCTCAATCATTGGTGTATGAGTGTCTTTGGGAAG 1110

Qy  1012 ATGAACAAGCTCATTAAGACGGTGTTGCATTGTTCTCTGCAGTATGGTCTCTGCTGGAACTCC 1071
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1111 ATGAACAAGCTCATTAAGACGGTGTTGCATTGTTCTCTGCAGTATGGTCTCTGCTGGAACTCC 1170

Qy  1072 ACCGTGAACCCCATCATCTATGCTTCTGAGGAGTAAGGAGGACCTGCGACACGGCTTTCCGGAGC 1131
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1171 ACCGTGAACCCCATCATCTATGCTTCTGAGGAGTAAGGAGGACCTGCGACACGGCTTTCCGGAGC 1230

Qy  1132 ATGTTTCCCTCTTGTGAAGGCACTGCGGCCTCTGCAGCCTCGATAACACGGCTTTCCGGAGC 1191
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1231 ATGTTTCCCTCTTGTGAAGGCACTGCGGCCTCTGCAGCCTCGATAACACAGCACGGGGGAC 1290

Qy  1192 TGCCTGGCACAAAAACACGGAAAACAAATGCAGCCAGTGTTCACAGGGCCCGGAGAAAGCTGCATC 1251
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1291 TGCCTGCACAAAACACGGAAAACAAATGCAGCCAGTGTTCCACAGGGCCCGGAGAAAGCTGCATC 1350

Qy  1252 AAGAGACACGGTCAAGATTGCCAAGGTAACCAAGTCTGTGTTCCACAGACACGTGCTGCCGAG 1311
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1351 AAGAGACACGGTCAAGATTGCCAAGGTAACCAATGTCTGTGTTCCACAGGACACGTGCTGCCGAG 1410

Qy  1312 GCTCTGTGA 1320
         |||||||||
Db  1411 GCTCTGTGA 1419
```

KW   G protein-coupled receptor; GPCR; drug screening; diagnosis;
KW   transgenic mouse; neurological disorder; adrenal gland disorder;
KW   colon disorder; intestinal disorder; cardiovascular disorder;
KW   muscular disorder; blood disorder; immune disorder; bone disorder;
KW   joint disorder; metabolic disorder; nutritive disorder; cancer;
KW   kidney disorder; liver disorder; lung disorder; breast disorder;
KW   ovary disorder; uterus disorder; prostate disorder; testis disorder;
KW   skin disorder; stomach disorder; pancreas disorder; spleen disorder;
KW   thymus disorder; thyroid disorder; antiinflammatory; antimanic;
KW   cytostatic; antiinflammatory; vasotropic; antiparkinsonian;
KW   CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
KW   virucide; hepatotropic; antibacterial; antianaemic; antiseborrheic;
KW   dermatological; antiulcer; antithyroid; antiallergic; anorectic;
KW   immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
KW   gene; 88.
XX
OS   Homo sapiens.
XX
PN   WO2004040000-A2.
XX
PD   13-MAY-2004.
XX
PF   09-SEP-2003; 2003WO-US028226.
XX
PR   09-SEP-2002; 2002US-0409303P.
PR   09-APR-2003; 2003US-0461329P.
XX
PA   (PRIM-) PRIMAL INC.
XX
PI   Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
PI   Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;
XX
DR   WPI; 2004-390329/36.
DR   P-PSDB; AD029261.
XX
PT   Novel mammalian G protein coupled receptors, useful for identifying
PT   compounds that modulates diagnosing and treating disease condition
PT   associated with GPCR dysfunction e.g. autoimmune diseases, angina
PT   pectoris, Parkinson's disease.
XX
PS   Claim 151; SEQ ID NO 951; 542pp; English.
XX
CC   The invention relates to human and mouse G protein-coupled receptors
CC   (GPCRs) and nucleic acids encoding them. The invention also relates to
CC   sequences at least 90% identical to the GPCR proteins and nucleic acids
CC   of the invention; methods of treating, preventing or diagnosing diseases
CC   associated with GPCRs of the invention; methods of screening for
CC   compounds useful in the treatment of GPCR-related diseases; a transgenic
CC   mouse comprising a GPCR gene of the invention; a mouse comprising a
CC   mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
CC   from the transgenic mice; kits comprising several mice, each of which has
CC   a mutation in a different GPCR gene of the invention; and kits comprising
CC   probes which hybridise to GPCR polynucleotides of the invention. The
CC   invention further discloses variants of the GPCR polypeptides and vectors
CC   comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
CC   be used in the diagnosis, treatment or prevention of a wide variety of
CC   diseases including neurological disorders (e.g., Alzheimer's disease,
CC   depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
CC   disorders of the adrenal gland; disorders of the colon or intestine
CC   (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
CC   syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
CC   myocardial infarction); muscular disorders (e.g., blood disorders (e.g.,
CC   anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
CC   AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
CC   arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
CC   obesity, enzyme deficiency-related diseases or vitamin deficiency-related
CC   diseases); and disorders of the kidney, liver, lung, breast, ovary,
CC   uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
CC   thyroid (e.g., cancer). The present sequence represents a GPCR-encoding
CC   nucleic acid of the invention. Note: The full sequence data for this
CC   patent did not form part of the printed specification; those sequences
CC   not shown were obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 1419 BP; 322 A; 409 C; 354 G; 334 T; 0 U; 0 Other;

Query Match   95.2%;   Score 1256.2;   DB 12;   Length 1419;
Best Local Similarity   99.4%;   Pred. No. 0;   Mismatches   8;   Indels   0;   Gaps   0;
Matches 1261;   Conservative   0;   Mismatches   8;   Indels   0;   Gaps   0;

```
Qy     52  ACTGACACCTCCTCGGAGAAGTCCCTTCCAAGAAGAAGATGACTGCGGAGGACAACCCCCAGCTA  111
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    151  ACTTCCTTTAGGGAGAAGTCCCTTCCAAGAAGAAGATGACTGCGGAGGACAACCCCCAGCTA  210

Qy    112  GTCCCAGCAGAGACCAGGTGAACATTACAGAATTTTACACAACAAGTCTCTCTGTCCTTCAAG  171
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    211  GTCCCAGCAGAGACCAGGTGAACATTACAGAATTTTACACAACAAGTCTCTCTGTCCTTCAAG  270

Qy    172  GAGAATGAGGAGAACATCCAGTTCATTCATGGACATAGAGTGTTTCATGGTC  231
               |||||||||||||||||||||||||||||||||||||||||
Db    271  GAGAATGAGGAGAACATCCAGTTCATTCATGGACATAGAGTGTTTCATGGTC  330

Qy    232  CTGAACCCCAGCCAGCAGCAGCTGGCCATTGTGCAGTCCTCAGCGTCTCAGCGTACCTTCACG  291
               ||||||||||||||||||||||||||||||||||||||||||||||||
Db    331  CTGAACCCCAGCCAGCAGCAGCTGGCCATTGTGCAGTCCTCAGCGTCTCAGCGTCACTTCACG  390

Qy    292  GTCCTGGAGAACCTCCTNGGTGCGTGTGGGCGTCATCCTCACCACTCCCGCAGCCTCCGCTGCAGG  351
               ||||||||||||||||||||||||||||||||||||||||||||||||
Db    391  GTCCTGGAGAACCTCCTNGGTGCGTGTGGGCGTCATCCTCACCACTCCCGCAGCCTCCGCTGCAGG  450

Qy    352  CCTTCCTTACCACTTCACCGGCAGCCTGCGGTGGGCAGAACCTCCTGGGGAGTGTCATTTTT  411
               |||||||||||||||||||||||||||||||||||||||||||||||
Db    451  CCTTCCTTACCACTTCACCGGCAGCCTGCGGTGGGCAGAACCTCCTGGGGAGTGTCATTTTT  510

Qy    412  GTCTACAGCTTCATTGACTTCCACGTGTTCCACCGCAAAGATAGCCCGCAAAGCGTGTTTCTG  471
               ||||||||||||||||||||||||||||||||||||||||||||||||
Db    511  GTCTACAGCTTCATTGACTTCCACGTGTTCCACCGCAAAGATAGCCCGCAAAGCGTGTTTCTG  570

Qy    472  TTCAAACTGGGTGGGGTGGGGTCACGGCCCTCCTTCACTGCCTCCTCCCGTGGGCCGCCTGTTCCTCACA  531
               |||||||||||||||||||||||||||||||||||||||||||||||||
Db    571  TTCAAACTGGGTGGGGTGGGGTCACGGCCCTCCTTCACTGCCTCCTCCCGTGGGCCAGCCTGTTCCTCACA  630

Qy    532  GCCATCGACAGGTACATATCCATTCACAGGCCCCTGCCTATAAGAGAGGATTGTCACCAGG  591
               |||||||||||||||||||||||||||||||||||||||||||||||||
Db    631  GCCATCGACAGGTACATATCCATTCACAGGCCCCTATAAGAGAGGATTGTCACCAGG  690

Qy    592  CCCAAGGCCGTGGTAGGGTTTTGCCTGATGTGGACCATAGCCATTGTGATCGCGTGGCTG  651
               ||||||||||||||||||||||||||||||||||||||||||||||||
Db    691  CCCAAGGCCGTGGTGGGGTTTTGCCTGATGTGGACCATAGCCATTGTGATCGCGTGGCTG  750

Qy    652  CCTCTCCTGGGGCTGGGAGAAACTGCAATCGTTGCTCAGACATTTTCCCACAC  711
               ||||||||||||||||||||||||||||||||||||||||||
Db    751  CCTCTCCTGGGGCTGGGAACTGCAATCGTTGCTCAGACATTTTCCCACAC  810

Qy    712  ATTGATGAAAACCTACCTGATGTTCTGAATCGGGGTCACCAGCGTACTGCTTCGTTCATC  771
               ||||||||||||||||||||||||||||||||||||||||||||||
Db    811  ATTGATGAAACCTACCTGATGTTCTGAATCGGGGTCACCAGCGTACTGCTTCGTTCATC  870

Qy    772  GTGTATGCGTACATGTATATTCTGGAAAGGCTCACAGCCACCACGCCGTCCGATGATTCAG  831
               ||||||||||||||||||||||||||||||||||||||||||||||
Db    871  GTGTATGCGTACATGTATATTCTGGAAAGGCTCACAGCCACCACGCCGTCCGATGATTCAG  930

Qy    832  CGTTGGCACCCAGAAGAGCATCATCCACACGTCTCGAGGATGGGGAAGGTACAGGTGACC  891
               ||||||||||||||||||||||||||||||||||||||||||||||
Db    931  CGTTGGCACCCAGAAGAGCATCATCCACACGTCTGAGGATGGGAAGGTACACAGGTGACC  990

Qy    892  CGGGCCAGAGCAAGCCCATGACAATTAGGTTAGCCAAGAGACCCTGGTCCTCGATCCTCGGTG  951
               |||||||||||||||||||||||||||||||||||||||||||||||
Db    991  CGGGCCAGAGCAAGCCCATGGACAATTAGGTTAGCCAAGAGACCCTGGTCCTCGATCCTCGGTG  1050

Qy    952  GTGTTGATCATCTGCTTGGGGCCCTCTCCTTGCAAATCATGGTTGTATGATGTCTTTGGGAAG  1011
               ||||||||||||||||||||||||||||||||||||||||||||||
Db   1051  GTGTTGATCATCTGCTCGGGGCCCTCGCTTGCAAATCATGGTGTATGATGTCTTTTGGGAAG  1110

Qy   1012  ATGAACAAGCTCATTAAGACGGGTGTTTGCATTCTCGCAGTATGCTTCTGCCTGAAACTCC  1071
               ||||||||||||||||||||||||||||||||||||||||||||||
Db   1111  ATGAACAAGCTCATTAAGACGGGTGTTTGCATTCTCGCAGTATGCTTGCCTGAAACTCC  1170
```

Db   1111 ATGAACAAGCTCATTAAGACGGGTGTTTGCATTCTCGCAGTATGCTTGCCTGAAACTCC 1170
Qy   1072 ACGGTGAACCCCATCATCTATGCTCTGAGGAGTAAGGACCTGCCGACAGCGTTTCCGGAGC 1131
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db   1171 ACGGTGAACCCCATCATCTATGCTCTGAGGAGTAAGGACCTGCCGACAGCGTTTCCGGAGC 1230

Qy   1132 ATGTTTCCCTCTTCTTGTGAAGGCACNGCCAGCCTCTTGGATAACACGATAGGGGGGGAC 1191
           ||||||||||||||||||||||||||||||||||||||||||||||
Db   1231 ATGTTTCCCTCTTCTTGTGAAGGCACTGCCAGCCTCTTGGATAACACAGATAGGGGGGAC 1290

Qy   1192 TGCCTGCACAAACAACGCAAACAATGCAGCGTGTTCACAGGGCGCCAGGAAGCTGCATC 1251
           ||||||||||||||||||||||||||||||||||||||||||||||
Db   1291 TGCCTGCACAAACAACGCAAACAATGCAGCCAGTGTTCACAGGGCGCCAGAAAGCTGCATC 1350

Qy   1252 AAGAGCACGGTCAAGATTGCCAAGGTAACCATATGTCTGTGTCCACAGACAGTCTCCGAG 1311
           ||||||||||||||||||||||||||||||||||||||||||||||
Db   1351 AAGAGACACAGTCAAGATTGCCAAGGTAACCATATGTCTGTGTCCACAGACAGTCTCCGAG 1410

Qy   1312 GCTCTGTGA 1320
           |||||||||
Db   1411 GCTCTGTGA 1419

RESULT 14
AB235604
ID   AB235604 standard; cDNA; 2135 BP.
XX
AC   AB235604;
XX
DT   05-FEB-2003   (first entry)
XX
DE   Human gene expression profile polynucleotide SEQ ID NO 715.
XX
KW   Human; artery; endothelium; umbilical; vein; aorta; pulmonary artery;
KW   bronchial epithelium; prostate; muscle; lung fibroblast; osteoblast;
KW   tumour; microarray; genome mapping; antibiotic; antiviral; antifungal;
KW   gene expression; gene; ss.
XX
OS   Homo sapiens.
XX
XX
PN   WO200274979-A2.
XX
PD   26-SEP-2002.
XX
XX
PF   20-MAR-2002; 2002WO-US008456.
XX
PR   20-MAR-2001; 2001US-0276947P.
XX
PA   (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
XX
PI   Wan J; Wang Y;
XX
DR   WPI; 2002-740862/80.
XX
PT   New gene expression profile generated from primary, endothelial,
PT   epithelial, and muscle cell types, useful for identifying disease
PT   pathologies involving alterations of gene expression, e.g. cancer.
XX
PS   Example 3; Page 818-819; 850pp; English.
XX
CC   The invention relates to a gene expression profile comprising one or more
CC   genes (ABZ34889-ABZ35692) and generated from a cell type. The cell type
CC   is a coronary artery endothelium, umbilical artery or vein endothelium,
CC   aortic endothelium, dermal microvascular endothelium, pulmonary artery
CC   endothelium, myometrium microvascular endothelium, keratinocyte
CC   epithelium, bronchial epithelium, mammary epithelium, prostate
CC   epithelium, renal cortical epithelium, renal proximal tubule epithelium,
CC   small airway epithelium, renal epithelium, umbilical artery smooth
CC   muscle, neonatal dermal fibroblast, pulmonary artery smooth
CC   muscle, mesangial cells, coronary artery smooth muscle,
CC   dermal fibroblast, neural progenitor cells, skeletal muscle, astrocytes,
CC   aortic smooth muscle, uterine smooth muscle, lung fibroblast,
CC   bronchial smooth muscle, mesangial cells, coronary artery smooth muscle,
CC   osteoblasts or prostate stromal cell. The gene expression profile is used

```
CC   for determining the level of RNA expression for a sample, determining the
CC   phenotype of a cell and distinguishing cell types. The gene or a protein
CC   expression profile is useful in identifying disease pathologies involving
CC   alterations of gene expression. The assessment of expression profiles may
CC   provide meaningful information with respect to tumour type and stage, and
CC   treatment methods, and prognosis. The gene or protein expression profile
CC   may also be used for creating microarrays. The microarray is useful for
CC   genetic and physical mapping of genomes, DNA sequencing, genetic or
CC   medical diagnosis, genotyping of organisms, confirming cell or tissue
CC   identifications and in identifying promising antibiotics, antiviral or
CC   antifungal agents
XX
SQ   Sequence 2135 BP; 537 A; 537 C; 482 G; 579 T; 0 U; 0 Other;

Query Match     95.2%;  Score 1256.2;  DB 6;  Length 2135;
Best Local Similarity   99.4%;  Pred. No. 0;
Matches 1261;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy     52 ACTGACCTCTCTGGGAGTCCCTTCCCTTCCAAGAGAAGAAGAATGACTGGGGGAGACAACCCCAGCCTA 111
          |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db    242 ACTTCCTTTAGGGGAAGTCCCTTCCAAGAGAAGAAGATGACTGGGGGAGACAACCCCAGCCTA 301

Qy    112 GTCCCAGCAGACGACCAGGTGAACATTACAGAATTTACAACAAGTCTCTCTCGTCCTTCAAG 171
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    302 GTCCCAGCAGACGACCAGGTGAACATTACAGAATTTACAACAAGTCTCTCTCGTCCTTCAAG 361

Qy    172 GAGAATGAGGAGGAGAACATTCAGTGTGGGGAGAACTTCATGGAACATAGAGCAATGGGTC 231
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    362 GAGAATGAGGAGGAGAACATTCAGTGTGGGGAGAACTTCATGGAACATAGAGCAATGGGTC 421

Qy    232 CTGAACCCCAGCCAGCAGCTGGCCATTGCAGTCCCTGTCCCTCACGCTGGGCCACCTTCACG 291
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    422 CTGAACCCCAGCCAGCAGCTGGCCATTGCAGTCCCTGTCCCTCACGCTGGGCCACCTTCACG 481

Qy    292 GTCCTCGGAGGAACCTCTGGGTGCTGTGGGCTCATCCTCCCACTCTCCGCCAGCCTCGCAGG 351
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    482 GTCCTCGGAGAACCTCTCTGGGTGCTGTGGGCTCATCCTCCCACTCTCCGCCAGCCTCGCAGG 541

Qy    352 CCTTCCTACCACTTCATCGGCAGCCTGCGCGTGCGAGAGCCTCCTGGGAGTGTCATTTTTT 411
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    542 CCTTCCTACCACTTCATCGGCAGCCTGCGCGTGCGAGAGCCTCCTGGGAGTGTCATTTTTT 601

Qy    412 GTCTACAGCTTCATTGACTTCACGTGTTCCACCGCAAAGAATAGCCCGCAACGTGTTTCTG 471
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    602 GTCTACAGCTTCATTGACTTCACGTGTTCCACCGCAAAGAATAGCCCGCAACGTGTTTCTG 661

Qy    472 TTCAAACTGGGCTGGGGGGTCAGGGCCTCCTTCACTGCCTCCGTGGGGCCAGCCTGTTCCTCACA 531
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    662 TTCAAACTGGGGTGGGGGTCAGGGCCTCCTTCACTGCCTCCGTGGGGCAGCCTGTTCCTCACA 721

Qy    532 GCCATCGACAGGTACATATCCAATCCAGGCCCCTGGGCCTATAAGAGGATTGGTCACCAGG 591
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    722 GCCATCGACAGGTACATATCCAATCCAGGCCCCTATAAGAGGATTGCTCACCAGG 781

Qy    592 CCCAAGGCCGTGTAGGGTTTTGCCTGACCATAGCCATTGTGATCCCCGTGCTG 651
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    782 CCCAAGGCCGTGGCGTTTGCCTGACTGAGTGGACCATAGCCATTGTGATCGGCGTGCTG 841

Qy    652 CCTCTCCTGGGGGTTGGAACTGCCGAAAACTGCAATCGTTTGCTCAGACCATTTTCCCACAC 711
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    842 CCTCTCCTGGGGGTTGGAACTGCCGAAAACTGCAATCGTTTGCTCAGACCATTTTCCCACAC 901

Qy    712 ATTGATGAAACCTACCTGAGTGTTCTGGATCGGGGATCACCACAGGGTACTGCTTCTGTCATC 771
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    902 ATTGATGAAACCTACCTGAGTGTTCGGATCGGGGGTCACCAGCGTACTGCTTCTGTCATC 961

Qy    772 GTGTATCCGTACATGTATATTCTCTGAGAAGGCTCACACGGCCAGCGTCCGCATGATTCAG 831
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    962 GTGTATCCGTACATGTATATTCTCTGGAAGGCTCACAGCCACCGCGTCCGCATGATTCAG 1021

Qy    832 CGTGGGCACCCAGAAGAGAGCATCATCCACACCGTCTCGAGGATCGGGAATCGGGAAGGTACAGGTGACC 891
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1022 CGTGGGCACCCAGAAGAGAGCATCATCCACACCGTCTCGAGGATCGGGAAGGTACAGGTGACC 1081

Qy    892 CGGCCAGACCAAGCCCCGCCATGGACATTAGGTTAGCCAAGACACCCTGGTTCCTGATCCTGGTG 951
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1082 CGGCCAGACCAAGCCCCGCCATGGACATTAGGTTAGCCAAGACACCCTGGTTCCTGATCCTGGTG 1141

Qy    952 GTGTTGATCATCTCTGCTGGGGGCCCTCTGCTTGCAATCATGGTGTATGATCTTTGGGAAG 1011
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1142 GTGTTGATCATCTCTGCTGGGGGCCCTCTGCTTGCAATCATGGTGTATGATCTTTGGGAAG 1201

Qy   1012 ATGAACAAGCTCATTAAGACGGTGTTTGCATTCTGCAGTATCCTGCTCCCTGTGAACTCC 1071
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1202 ATGAACAAGCTCATTAAGACGGTGTTTGCATTCTGCAGTATCCTGCTCCCTGTGAACTCC 1261

Qy   1072 ACCGTGAACCCCATCACTCTATGCTCTCGAGGAGTAAGGACCTGCGGACAGCGCTTTCCCGGAGC 1131
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1262 ACCGTGAACCCCATCACTCTATGCTCTCGAGGAGTAAGGACCTGCGGACACGCGCTTTCCCGGAGC 1321

Qy   1132 ATGTTTCCCTCTTGTGAAGGCACTCGCGCAGCCTTCTGGATAAACAGCATGGGGGGGACTCGGAC 1191
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1322 ATGTTTCCCTCTTGTGAAGGCACTCGCGCGGCCGCCTTCTGGATAAACAGCATGGGGGGACTCGGAC 1381

Qy   1192 TGGCCTGCACAAACACGCAGAAACAATGCAGCCCACTGTTCACAGGGCGCCGAGAAAAGCTGCATC 1251
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1382 TGGCCTGCACAAACACGCAGAAACAATGCAGCCCACTGTTCACAGGGGCGCCGAGAAAAGCTGCATC 1441

Qy   1252 AAGAGCACGGTCAAGATTGCCAAGGTAACCATTGTCTGTCCTCACAGGACGCCGAGGTCTGCCCGAG 1311
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1442 AAGAGCACAGTCAAGATTGCCAAGGTAACCATTGTCTGTCCTCACAGGACGTCTGACGGTCTGCCCGAG 1501

Qy   1312 GCTCTGTGA 1320
          |||||||||
Db   1502 GCTCTGTGA 1510
```

```
CC   array element in a microarray for monitoring the expression of a number
CC   of target polynucleotides. The microarray is particularly useful in the
CC   diagnosis and treatment of cancer and immunopathology and neuropathology.
CC   The microarray is useful in diagnostics and treatment regimens, drug
CC   discovery and development, toxicological and carcinogenicity studies,
CC   forensics and pharmacogenomics. The microarray is also useful for
CC   monitoring progression of diseases and for developing sophisticated
CC   profiles for the effects of currently available therapeutic drugs. The
CC   combination is also useful for purifying a subpopulation of mRNAs, cDNAs
CC   and genomic fragments and in research and diagnostic applications. The
CC   array can detect changes in expression in a large number of genes coding
CC   for different signaling pathway populations which can be used to diagnose
CC   various diseases including cancer e.g. adenocarcinoma and leukaemia,
CC   immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease
CC   and Parkinson's disease. The present sequence represents a polynucleotide
CC   probe of the invention. Note: The sequence data for this patent did not
CC   form part of the printed specification but was obtained in electronic
CC   format directly from USPTO at
CC   seqdata.uspto.gov/sequence.html?DocID=06500938B1
XX
SQ   Sequence 2135 BP; 537 A; 537 C; 482 G; 579 T; 0 U; 0 Other;

Query Match             95.2%;  Score 1256.2;  DB 10;  Length 2135;
Best Local Similarity   99.4%;
Matches 1261;  Conservative   0;  Mismatches   8;  Indels   0;  Gaps   0;

Qy         52 ACTGACACCCTCCTCGGAAGTCCCTTCCAAGAGAAGATGACTGCGGAGACAACCCCCAGCTA 111
              |||    ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 ACTTCCTTTAGGGGAAGTCCCTTCCAAGAGAAGATGACTGCGGAGACAACCCCCAGCTA 301

Qy        112 GTCCCAGCAGACCAGGTGAACATTACAGAATTTTACAACAAGTCTCTCGTCCTTCAAG 171
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 GTCCCAGCAGACCAGGTGAACATTACAGAATTTTACAACAAGTCTCTCGTCCTTCAAG 361

Qy        172 GAGAATGAGGAGGAACATCCAGTGTGGGGGAGAACTTCATGGACATAGAGTGTTTCATGGTC 231
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 GAGAATGAGGAGGAACATCCAGTGTGGGGGAGAACTTCATGGACATAGAGTGTTTCATGGTC 421

Qy        232 CTGAACCCCAGCCAGCAGCTGGCCATTGCAGTCCTGTCCTCACGCTGGGCACCTTCACG 291
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 CTGAACCCCAGCCAGCAGCTGGCCATTGCAGTCCTGTCCTCACGCTGGGCACCTTCACG 481

Qy        292 GTCCCTGGAGAACCTCCTCGGGTGCGTGGGTCATCCTCCACTCCCGGCGCCTCCGGCTGGCAGG 351
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        482 GTCCCTGGAGAACCTCCTCGGGTGCGTGGGTCATCCTCCACTCCCGGCGCCTCCGGCTGGCAGG 541

Qy        352 CCTTCCTTACCACTTCATCGGCAGCCGGTGGCAGGACCTCCTGGGGAGTGTCATTTTT 411
              ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        412 GTCTACAGCTTCATTGACTTCCACGTGTTCCACCGCAAAGATAGCCCGCAACCGTGTTTCTG 471
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        602 GTCTACAGCTTCATTGACTTCCACGTGTTCCACCGCAAAGATAGCCCGCAACCGTGTTTCTG 661

Qy        472 TTTCAAACTGGGTGGGGTCACGGCCCTCCTTCACTGCCTCCGGTGGGCAGCCGTTCCTCACA 531
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        662 TTTCAAACTGGGTGGGGTCACGGCCCTCCTTCACTGCCTCCGGTGGGCAGCCGTTCCTCACA 721

Qy        532 GCCATCGACAGGTACATATCCATTCACAGGCCCCTGCCTATAAGAGGATTGTCACCAGG 591
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        722 GCCATCGACAGCAGTACATATCCATTCACAGGCCCCTGCCTATAAGAGGATTGTCACCAGG 781

Qy        592 CCCAAGGCCGTGGTAGGGTTTTGCCTGATGTGGACCATAGCCATTGTCCCGGTGCTG 651
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 CCCAAGGCCGTGGTAGGGTTTTGCCTGATGTGGACCATAGCCATTGTCCCGGTGCTG 841

Qy        652 CCTCTCTGGGAGAAACTGCAAATCTGTTTGCTCAGACACATTTCCCACAC 711
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Db        842 CCTCTCTGGGCTGGGAACTGCAAATCTGTTTGCTCAGACACATTTCCCACAC 901

Qy        712 ATTGATGAAAACCTACCTGAGTTCTGGAATCGGGGGTCACCCAGGTACTGCTTCGTTCATC 771
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        772 GTGTATGCGTACATGTATATTCTCTGGAAGGCTCACAGCGGCCTTCGGGATTCAG 831
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Qy        832 CGTGGCACCCGAGAGAGCATCATCATCCACACGTCTGAGGATGGGAAGGTACAGGTGACC 891
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Db       1022 CGTGGCACCCGAGAGAGCATCATCATCCACACGTCTGAGGATGGGAAGGTACAGGTGACC 1081

Qy        892 CGGGCCAGACCAAGCCCGCATGGACATTAGGTTAGGCCAAGGACCCTGGGTCCTGGGTG 951
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1082 CGGGCCAGACCAAGCCCGCATGGACATTAGGTTAGGCCAAGGACCCTGGGTCCTGGGTG 1141

Qy        952 GTGTTGATCATCTGCTGGGGCCCCTCCTGCTTGCAATCATGGTGTATGATGGTCCTGGAAG 1011
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1142 GTGTTGATCATCTGCTGGGGCCCCTCCTGCTTGCAATCATGGTGTATGATGGTCCTGGAAG 1201

Qy       1012 ATGAACAAGCTCATTAAGACGGGTGTTTGCATTCTTGCAGTATGCCTCCTGCTGAAACTCC 1071
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Db       1202 ATGAACAAGCTCATTAAGACGGGTGTTTGCATTCTTGCAGTATGCCTCCTGCTGAAACTCC 1261

Qy       1072 ACCGTGAACCCCATCCATCTCATTAATGCTCTCGAGGAGTAAGGACCTGCGACACACGC 1131
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Db       1262 ACCGTGAACCCCATCATTCATTAATGCTCTCGAGGAGTAAGGACCTGCGACACACGC 1321

Qy       1132 ATGTTTTCCCTCTTGTTGAAGGCACTGCGCAGCCCTCTGGATAACACCATGGGGGGAGAC 1191
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Qy       1192 TGCCTGCACAAAACACGCAAAACAATGCAGCCAGTGTTCACAGGGGCGCGAGAAAGCTGCATC 1251
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Db       1382 TGCCTGCACAAAACACGCAAAACAATGCAGCCAGTGTTCACAGGGGCGCGAGAAAGCTGCATC 1441

Qy       1252 AAGAGCACGGTCAAGATTGCCAAGGTAACCATGTGTCGTGTCCACAGACACGTCTGCCGAG 1311
              |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1442 AAGAGCACAGTCAAGATTGCCAAGGTAACCATGTGTCGTGTCCACAGACACGTCTGCCGAG 1501

Qy       1312 GCTCTGTGA 1320
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Db       1502 GCTCTGTGA 1510
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Search completed: June 16, 2006, 23:47:30
Job time : 842 secs

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OM nucleic - nucleic search, using sw model

                        GenCore version 5.1.9
                        Copyright (c) 1993 - 2006 Bioacceleration Ltd.

Run on:             June 16, 2006, 23:31:30 ; Search time 6937 Seconds
                         (without alignments)
                         10640.553 Million cell updates/sec

Title:              US-10-521-428A-1
Perfect score:      1320
Sequence:           1 atgaagtcgatcctagatgg...........cgtctgccgaggcctgtga 1320

Scoring table:      IDENTITY_NUC
                    Gapop 10.0 , Gapext 1.0

Searched:           48236798 seqs, 2795665780 residues

Total number of hits satisfying chosen parameters:    96473596

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        EST:*

                  1:  gb_est1:*
                  2:  gb_est3:*
                  3:  gb_est4:*
                  4:  gb_est5:*
                  5:  gb_est6:*
                  6:  gb_htc:*
                  7:  gb_est2:*
                  8:  gb_est7:*
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                 13:  gb_gss3:*
                 14:  gb_gss4:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	Match DB	DB ID	Description
1	1257.8	95.3	1419	14	AY415602	AY415602 Homo sapi
2	1048	79.4	1422	14	AY415604	AY415604 Mus muscu
3	1048	79.4	1642	6	AK139417	AK139417 Mus muscu
4	804.2	60.9	821	14	AY415603	AY415603 Pan trogl
5	639.8	48.5	769	4	DN533141	DN533141 1361255 M
6	634.2	48.0	752	4	CA327850	CA327850 UI-M-FY0-
7	630.4	47.8	737	4	CA328435	CA328435 UI-M-FY0-
8	616.2	46.7	717	10	DY320503	DY320503 AGENCOURT
9	602.8	45.7	844	4	CB244710	CB244710 UI-M-FY0-
10	599.8	45.4	737	5	CF533059	CF533059 UI-M-FY0-
c 11	592.2	44.9	774	8	CO959553	CO959553 AGENCOURT
c 12	592.2	44.9	1151	12	CC202312	CC202312 CH261-70E
c 13	577.6	43.3	680	9	DN515498	DN515498 1252753 M
14	571	43.3	780	4	BU705501	BU705501 UI-M-FO0-
c 15	570.8	43.2	789	4	CB520209	CB520209 UI-M-GIO-
16	565.4	42.8	567	9	DA720992	DA720992 DA720992
17	539.6	40.9	664	9	DN531749	DN531749 1359719 M
18	534.8	40.5	634	4	CB244673	CB244673 UI-M-FY0-
19	527.6	40.0	722	9	DR001597	DR001597 TC111611
20	524.6	39.7	844	3	BU340323	BU340323 603518766
21	521.2	39.5	772	3	BU385874	BU385874 603856179
22	517.4	39.2	775	3	BU383885	BU383885 603584117
23	516.2	39.1	938	3	BU252543	BU252543 603413268
24	511.8	38.8	644	4	CA327351	CA327351 UI-M-FY0-
25	509.8	38.6	732	4	CA329114	CA329114 UI-M-FY0-
26	493.2	37.4	599	5	CD352210	CD352210 UI-M-GI0-
27	483.8	36.7	812	3	BU338912	BU338912 603133771
28	474.2	35.9	756	3	BU370895	BU370895 603159001
29	471.4	35.7	999	3	BU370225	BU370225 603596892
30	463.4	35.1	687	3	BU370225	BU370225 603596892
31	456.8	34.6	632	5	CD351932	CD351932 UI-M-GI0-
32	448.6	34.0	781	3	BU142725	BU142725 603136386
33	447.2	33.9	635	3	CN602609	CN602609 C0067841
34	443.4	33.6	648	3	BU267937	BU267937 603506854
35	443	33.6	826	5	CF538061	CF538061 UI-M-GI0-
36	433.2	32.8	643	3	BU447747	BU447747 604146524
37	431.8	32.7	742	3	CF723449	CF723449 UI-M-GV0-
c 38	431.4	32.7	555	2	BI134232	BI134232 UI-M-BH3-
39	417	31.6	889	10	DR428823	DR428823 nax08b07.
40	414.4	31.4	834	10	DT237605	DT237605 JGI_CAAT9
41	405.4	30.7	709	8	CO959554	CO959554 AGENCOURT
42	402.6	30.5	646	4	CB520408	CB520408 UI-M-GI0-
c 43	402.6	30.5	1138	12	CC218820	CC218820 CH261-69E
c 44	402.2	30.5	712	9	DN514830	DN514830 1251985 M
c 45	389.4	29.5	457	7	AW489878	AW489878 UI-M-BH3-

ALIGNMENTS

RESULT 1
AY415602

LOCUS   AY415602   1419 bp   DNA   linear   GSS 17-DEC-2003
DEFINITION Homo sapiens CNR1 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY415602
VERSION   AY415602.1 GI:39771561
KEYWORDS   GSS.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 1419)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE   Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
  PUBMED   14671302
REFERENCE   2 (bases 1 to 1419)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE   Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Guide Drive,
            Rockville, MD 20850, USA
COMMENT   This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES   Location/Qualifiers
     source   1..1419
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene   <1..>1419
                     /gene="CNR1"
                     /locus_tag="HCM5612"
ORIGIN
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Query Match   95.3%;   Score 1257.8;   DB 14;   Length 1419;
Best Local Similarity   99.4%;   Pred. No. 0;   Mismatches 7;   Indels 0;   Gaps 0;
Matches 1262;   Conservative 0;

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Qy      52 ACTGACCTCTGGGAAGTCCCTTCCAAGAGAAGATGACTGCGGGAGAAGCAACCCCCAGCTA 111
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Db     151 ACTTCCTTCAGGGGTAGTCCCTTCCAAGAAATTTTACAACAAGTCTCTTCTTCGGTCCTTCAAG 210

Qy     112 GTCCCAGCAGACCAGGTGAACATTACAGAGAATTTTACAACAACAGTCTCTTCGGTCCTTCAAG 171
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     211 GTCCCAGCAGACCAGGTGAACATTACAGAGAATTTTACAACAACAGTCTCTTCGGTCCTTCAAG 270

Qy     172 GAGAATGAGGAGGAACATCAGTGTGGGGGAGAACTTCATGGACTAGAGTGTTTCATCGGTC 231
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     271 GAGAATGAGGAGGAACATCAGTGTGGGGGAGAACTTCATGGACTAGAGTGTTTCATCGGTC 330

Qy     232 CTGAACCCCAGCCAGCAGCTGGCCATTGCAGTCTCGCGCTGGGCACCTTCACG 291
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Db     331 CTGAACCCCAGCCAGCAGCTGGCCATTGCAGTCTCGCGCTGGGCACCTTCACG 390

Qy     292 GTCCCTGGAGAACCTCCTCGGTGGTGGTGGGTGGTGGTCAATCCTCCTTCCGCTGCAGG 351
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     391 GTCCCTGGAGAACCTCCTCGGTGCTGGTGGGTCAATCCTCCTTCCGCTGCAGG 450

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Db     451 CCTTCCTTACCACTTCATCGGCGAGCGCTTGGCGTGGGGCAGAGCTTCCTCGGGAGTGTCATTTTT 510

Qy     412 GTCTCTACAGCTTCATTGACTTCCACGTGTTCCACGCGCAAAGATAGTGTTTCTG 471
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     511 GTCTCTACAGCTTCATTGACTTCCACGTGTTCCACGCGCAAAGATAGTGTTTCTG 570

Qy     472 TTCAAACTGGGTGGGGTGGGGTCACGGCGGCCGCCTCCACTCCGCTGGGGCACCTGCAGG 531
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     571 TTCAAACTGGGTGGGGTGGGGTCACGGCGGCCGCCTCCACTCCGCTGGGGCACCTGCAGG 630

Qy     532 GCCATCGACAGTACATATCAATTCACAGGCCCCCTGGCCTATAAAGAGGATTGTCACCAGG 591
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Db     631 GCCATCGACAGTACATATCAATTCACAGGCCCCCTGGCCTATAAAGAGGATTGTCACCAGG 690

Qy     592 CCCAAGGCCGTGGTAGGCGTTTGGCCTGATGTGGACCATAGCCATTGTGATCGGCCGTGCTG 651
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     691 CCCAAGGCCGTGGTAGGCGTGGCGTTTGGCCTGATGTGGACCATAGCCATTGTGATCGGCCGTGCTG 750

Qy     652 CCTCTCCTGGGGGCTGGGAGAAAACTGCAATCTGTTGTTGCTCGAAGCCATTTTCCCACAC 711
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Qy     712 ATTGATGAAAACCTACCTGATGTTCTCGATCGGGGTCGGGGTCACCGACTACTCGTTCATC 771
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Db     811 ATTGATGAAAACCTACCTGATGTTCTCGATCGGGGTCGGGGTCACCGACTACTCGTTCATC 870

Qy     772 GTGTAATCGGTACATGTATATTCTTCTGGAAGGCTCACAGCCACGGGTCCGCATGATTCAG 831
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Db     871 GTGTAATCGGTACATGTATATTCTTCTGGAAGGCTCACAGCCACGGGTCCGCATGATTCAG 930

Qy     832 CGTGGCACCCAGAAGAGAGCATCACATCCACACCTCTGAGGATGGGAAGGTACAGGTGACC 891
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     931 CGTGGCACCCAGAAGAGAGCATCACATCCACACCTCTGAGGATGGGAAGGTACAGGTGACC 990

Qy     892 CGGCCCAGACCCAAGCCCCATGGACATTAGGTTAGCCAAGAACCCTCGGTCCTCTGATCCTCGGTG 951
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Db     991 CGGCCCAGACCCAAGCCCCATGGACATTAGGTTAGCCAAGAACCCTCGGTCCTCTGATCCTCGGTG 1050

Qy     952 GTGTTGATCATCTGCTGGGCCCTCGCTTGCAATCATGGTGTATGAGTGTCTTGGGAAG 1011
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1051 GTGTTGATCATCTGCTGGGCCCTCGCTTGCAATCATGGTGTATGAGTGTCTTGGGAAG 1110

Qy    1012 ATGAACAAGCTCATTAAGACGGGTGTTTGCATTCTGCTGCTGCTGCTGAACTCC 1071
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Db    1111 ATGAACAAGCTCATTAAGACGGGTGTTTGCATTCTGCTGCTGCTGAACTCC 1170

Qy    1072 ACCGGTGAACCCATCATCTATGCTCTGCGAGGAGTRAGGACCTGCGGACACGGCTTTCCGGGAGC 1131
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Db    1131
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RESULT 2
AY415604

LOCUS   AY415604   1422 bp   DNA   linear   GSS 17-DEC-2003
DEFINITION   Mus musculus CNR1 gene, VIRTUAL TRANSCRIPT, partial sequence,
             genomic survey sequence.
ACCESSION   AY415604
VERSION   AY415604.1   GI:39771563
KEYWORDS   GSS.
SOURCE   Mus musculus (house mouse)
  ORGANISM   Mus musculus
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
             Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 1422)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
             Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
             Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
             Adams,M.D. and Cargill,M.
  TITLE   Inferring nonneutral evolution from human-chimp-mouse orthologous
             gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2 (bases 1 to 1422)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
             Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
             Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
             Adams,M.D. and Cargill,M.
  TITLE   Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
             Rockville, MD 20850, USA
COMMENT   This sequence was made by sequencing genomic exons and ordering
             them based on alignment.
FEATURES   Location/Qualifiers
     source   1..1422
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Matches 1139;   Conservative 0;   Mismatches 130;

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Qy     112 GTCCCAGC---AGACCAGGTGAACATTACAGAGAATTTTACAACAAGTCTCTTCTTCGGTCCTTC 168
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Db    871 ATTGTGTATGCATCACATTGTCATCCCTCTGGAAGCCTCACAGCCGCCCGTCGCCATGATC  930

Qy    829 CAGGCCTTCCCTGGGGCTGGGAACTGCTGCCCAGAAGAGATGGGGAAGGTACAGGTG  888
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Qy    889 ACCCGGCCAGCACCAAGCCCGATGGACACCGCCCGCCCGCCCGATG  948
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RESULT 3
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DEFINITION Mus musculus 10 days neonate cortex cDNA, RIKEN full-length
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ACCESSION   AK139417
VERSION   AK139417.1 GI:74228276
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REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE   High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE   Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
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            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
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            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE   RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
   PUBMED   11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
            Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
            Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
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            Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
            Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
            Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
            Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
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            Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
            Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C.A., Wilming,L.,
            Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
            and Hayashizaki,Y.
  CONSRTM   RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium
  TITLE   Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409 (6821), 685-690 (2001)
   PUBMED   11217851
REFERENCE   5

AUTHORS   Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
          Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
          Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
          Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
          Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
          Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
          Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
          Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
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          Rogers,J., Birney,E. and Hayashizaki,Y.
  CONSRTM   FANTOM Consortium
  TITLE   Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420 (6915), 563-573 (2002)
  PUBMED   12466851
REFERENCE   6
  AUTHORS   Carninci,P., Kasukawa,T., Katayama,S., Gough,J., Frith,M.C.,
            Maeda,N., Oyama,R., Ravasi,T., Lenhard,B., Wells,C., Kodzius,R.,
            Shimokawa,K., Bajic,V.B., Brenner,S.E., Batalov,S., Forrest,A.R.,
            Zavolan,M., Davis,M.J., Wilming,L.G., Aidinis,V., Allen,J.E.,
            Ambesi-Impiombato,A., Apweiler,R., Aturaliya,R.N., Bailey,T.L.,
            Bansal,M., Baxter,L., Beisel,K.W., Bersano,T., Bono,H., Chalk,A.M.,
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            Crowe,M.L., Dalla,E., Dalrymple,B.P., de Bono,B., Della Gatta,G.,
            di Bernardo,D., Down,T., Engstrom,P., Fagiolini,M., Faulkner,G.,
            Fletcher,C.F., Fukushima,T., Furuno,M., Futaki,S., Gariboldi,M.,
            Georgii-Hemming,P., Gingeras,T.R., Gojobori,T., Green,R.E.,
            Gustincich,S., Harbers,M., Hayashi,Y., Hensch,T.K., Hirokawa,N.,
            Hill,D., Huminiecki,L., Iacono,M., Ikeo,K., Iwama,A., Ishikawa,T.,
            Jakt,M., Kanapin,A., Katoh,M., Kawasawa,Y., Kelso,J., Kitamura,H.,
            Kitano,H., Kollias,G., Krishnan,S.P., Kruger,A., Kummerfeld,S.K.,
            Kurochkin,I.V., Lareau,L.F., Lazarevic,D., Lipovich,L., Liu,J.,
            Liuni,S., McWilliam,S., Madan Babu,M., Madera,M., Marchionni,L.,
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            Ng,P., Nilsson,R., Nishiguchi,S., Nishikawa,S., Nori,F., Ohara,O.,
            Okazaki,Y., Orlando,V., Pang,K.C., Pavan,W.J., Pavesi,G.,
            Pesole,G., Petrovsky,N., Piazza,S., Reed,J., Reid,J.F., Ring,B.Z.,
            Ringwald,M., Rost,B., Ruan,Y., Salzberg,S.L., Sandelin,A.,
            Schneider,C., Schonbach,C., Sekiguchi,K., Semple,C.A., Seno,S.,
            Sessa,L., Sheng,Y., Shibata,Y., Shimada,H., Shimada,K., Silva,D.,
            Sinclair,B., Sperling,S., Stupka,E., Sugiura,K., Sultana,R.,
            Takenaka,Y., Taki,K., Tammoja,K., Tan,S.L., Tang,S., Taylor,M.S.,
            Tegner,J., Teichmann,S.A., Ueda,H.R., van Nimwegen,E., Verardo,R.,
            Wei,C.L., Yagi,K., Yamanishi,H., Zabarovsky,E., Zhu,S., Zimmer,A.,
            Hide,W., Bult,C., Grimmond,S.M., Teasdale,R.D., Liu,E.T.,
            Brusic,V., Quackenbush,J., Wahlestedt,C., Mattick,J.S., Hume,D.A.,
            Kai,C., Sasaki,D., Tomaru,Y., Fukuda,S., Kanamori-Katayama,M.,
            Suzuki,M., Aoki,J., Arakawa,T., Iida,J., Imamura,K., Itoh,M.,
            Kato,T., Kawaji,H., Kawagashira,N., Kawashima,T., Kojima,M.,
            Kondo,S., Konno,H., Nakano,K., Ninomiya,N., Nishio,T., Okada,M.,
            Plessy,C., Shibata,K., Shiraki,T., Suzuki,S., Tagami,M., Waki,K.,
            Watahiki,A., Okamura-Oho,Y., Suzuki,H., Kawai,J. and Hayashizaki,Y.
  CONSRTM   FANTOM Consortium
  TITLE   The transcriptional landscape of the mammalian genome
  JOURNAL   Science 309 (5740), 1559-1563 (2005)

REFERENCE   7
  PUBMED   16141072
  AUTHORS   Katayama,S., Tomaru,Y., Kasukawa,T., Waki,K., Nakanishi,M.,
            Nakamura,M., Nishida,H., Yap,C.C., Suzuki,M., Kawai,J., Suzuki,H.,
            Carninci,P., Hayashizaki,Y., Wells,C., Frith,M., Ravasi,T.,
            Pang,K.C., Hallinan,J., Mattick,J., Hume,D.A., Lipovich,L.,
            Batalov,S., Engstrom,P.G., Mizuno,Y., Faghihi,M.A., Sandelin,A.,
            Chalk,A.M., Mottagui-Tabar,S., Liang,Z., Lenhard,B. and
            Wahlestedt,C.
  CONSRTM   RIKEN Genome Exploration Research Group
  TITLE   Antisense transcription in the mammalian transcriptome
  JOURNAL   Science 309 (5740), 1564-1566 (2005)
  PUBMED   16141073
REFERENCE   8 (bases 1 to 1642)
  AUTHORS   Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K.,
            Hori,F., Iida,J., Imamura,K., Imotani,K., Itoh,M., Kanagawa,S.,
            Kawai,J., Kojima,M., Kono,H., Murata,M., Nakamura,M., Ninomiya,N.,
            Nishiyori,H., Nomura,K., Ohno,M., Sakazume,N., Sano,H., Sasaki,D.,
            Shibata,K., Shiraki,T., Tagami,M., Tagami,Y., Waki,K., Watahiki,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE   Direct Submission
  JOURNAL   Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa, 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT   cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.jp/.
            URL:http://fantom.gsc.riken.jp/.
FEATURES   Location/Qualifiers
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ORIGIN
Qy   52 ACTGACCTCCTGGGAAGTCCCTTCCAAGAGAAGATGACTGCGGGAGACAACCCCAGCTA 111
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Qy   Query Match   79.4%;   Score 1048;   DB 6;   Length 1642;
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             Matches 1139; Conservative 0; Mismatches 130; Indels 3; Gaps 1;

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Qy   409 TTTGTCTACAGCTTCATTGACTTCCCACGTGTTCCACCGGCCAAAGATAGCCGCAACGTGTTT 468
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db   708 TTTGTCTACAGCTTTGTTGACTTCCACGTGTTCCACCCGCCAAAGATAGTCCCAATGTGTTTT 767

Qy   469 CTGTTCAAACTGGGGTGGGGGTCACGGCCTCCTTCCTTCACTCCCGTTGGGGCCAGCCTCCGTTCCTC 528
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db   768 CTGTTCAAACTGGGGTGGGGTTACCGGCCTTCTCCTTTCACTCCTGTGGGGGCAGCCTCTGTTCCTC 827

Qy   529 ACAGCCATCGACAGGTACATATCCATTCACAGCCCCCTGGCCCTTATTAAGCAGGATTGTCACC 588
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   828 ACGGCCATCGACAGGTACATATCCATTCACAGGCCCTTATAAGAGGATCGTCACC 887

Qy   589 AGGCCCAAGGCCGTGTAGCGTTTTGCCTGATGTGGACCATTAGCCATTGTGATCGCCGTG 648
         ||||||||||||||||||||||||||||||||||||||||||||||||
Db   888 AGGCCCAAGGCCGTAGTGGCCTTTTTGCTTGATGTGGAC TATTGCCTATTGTTTGCTCAAATGCTG 947

Qy   649 CTGCCTTCCTGGGCTGGAGAAACTGCCAATCTCTGTTGCTCAGACATTTTCCCA 708
         ||||||||||||||||||||||||||||||||||||||||
Db   948 TTGCCCTCTGGGCTGGAACTGCAAGAAGCTGCAATCTGTTTGCTCAGACAATCTTCCCA 1007

Qy   709 CACATTGATGAAACCTACCCTGATGTTCTTGGGATCGGGGTACTGCTTCTCTGTTC 768
         ||||||||||||||||||||||||||||||||||||||
Db  1008 CTCGTTGATGAAAACCTACCCTGATGTTCTGGAGTCACCAGTGCTGTTGCTGTTC 1067

Qy   769 ATCGGTGTATGGGTACATGTATATTCTCTGGAAGGCTCACAGCGCCACCGCGCCTCCGGCATGATT 828
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Db  1068 ATTGTGTGTATGCATACATTCTCTGGAAGGCTCACAGCGCCACCGCACGATC 1127

Qy   829 CAGCGGTGGCCACCCAGAGAGCATCATCATCATCACAGTCTGAGGATGGGGAAGGTTACAGGTG 888
         |||||||||||||||||||||||||||||||||||||
Db   888 CAGCGGTGGAACCCAGAAAGCATCATCATCATTCAGACACTTCAGAAGAGATGGCCAAGGTG 888

Qy   889 ACCCGGCCAGACCAAGCCCGCATGGACATTAGGTTAGGTTACCCAGACCCTGGTTCTTCCTGGTC 948
         ||||||||||||||||||||||||||||||||||||||
Db  1128 CAGGCGGTGGAACCCAGAAAAGCATCATCATTCAGAAGATGGCCAAGGTGCAGGGTG 1187

Qy   949 GTGGGTGTTGATCATCTGCTCGGGGCCCCTCGCTGTTGCTTCGCAATCATGGTGTATGATGTCTTTGGG 1008
         ||||||||||||||||||||||||||||||||||||||
Db  1248 GTGGGTGTTGATCATCTGCTGGGGGCCCCTCGCTGATCACGGTGTGATGATGTCTTTGGG 1307

Qy  1009 AAGATGAAACAAGCTCATTAAGACGGTGTTTGCAATTCTGCAGTATGCTCTGCCTGCTGCTGAAC 1068
         ||||||||||||||||||||||||||||||||||||||
Db  1068 ATTGTGATGACAGTACAATTCTCTGGAAGGCTCACAGCGCCACCGCACGATC 1127

Qy  1069 TCCACCCGTGAACCCCATCATCTATGCTCTGCGAAGTCCGACACCGGCTTTCCGG 1128
         ||||||||||||||||||||||||||||||||||||||
Db  1128 CAGCGGTGGAACCCAGAAAAGCATCATCATTCAGAAGATGGCCAAGGTGCAGGGTG 1187

Qy  1128 CAGGCGGTGGAACCCAGAAAAGCATCATCATTCAGAAGATGGCCAAGGTG 1187
         ||||||||||||||||||||||||||||||||||||||
Db  1308 AAGATGAAACAAGCTTATCAGACGGTGTTTGCCTTCTGCAGTATGCTCTGCCTGCTGAAC 1367

Qy  1188 ACACGGCCTGACCAAGCCCGCATGGACATTAGGTTACCCAGACCCTGGTTCTTGGATCCTG 1247
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Db  1368 TCCACCCTGAACCCCATCATCTATGCTCTGCGGAGCAAGGACCTGCGGCATGCTTTCCGC 1427

Qy  1248 GTGGGTGTTGATCATCTGCTCGGGGCCCCTCGCTGATCACGGTGTGATGATGTCTTTGGG 1307
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Db  1428 AGCATGTTCCCTTCATGTGAAGGCACTGGGCAGCCCTCCTAGATAACACCATGGGGGGGGACTCA 1487

Qy  1308 AAGATGAAACAAGCTTATCAGACGGTGTTTGCCTTCTGCAGTATGCTCTGCCTGCTGAAC 1367

Qy  1368 TCCACCCTGAACCCCATCATCTATGCTCTGCGGAGCAAGGACCTGCGGCATGCTTTCCGC 1427

Db  1129 AGCATGTTCCCTTCATGTGAAGGCACTGGGCAGCCCTCCTAGATAACACCATGGGGGGGGACTCA 1188

Qy  1428 AGCATGTTCCCTTCATGTGAAGGCACTGGGCAGCCCTCCTAGATAACACCATGGGGGGGGACTCA 1487
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RESULT 4

AY415603

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LOCUS       AY415603               821 bp    DNA     linear   GSS 17-DEC-2003
DEFINITION  Pan troglodytes CNR1 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY415603
VERSION     AY415603.1  GI:39771562
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1  (bases 1 to 821)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 821)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1..821
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
     gene            <1..>821
                     /gene="CNR1"
                     /locus_tag="HCMS612"
ORIGIN

Query Match     60.9%;  Score 804.2;  DB 14;  Length 821;
Best Local Similarity   98.2%;
Matches  806;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;
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Qy  1189 GACTGCCTGCCAGAACAAAACACACCCCAAAACAAATGCAGCCCAGTGTTCACAGGGGCCCCAGAGAAAGCTGC 1248
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Db  1488 GACTGCCTGCCAGAACAACACCCCAATAACACAGCCCAGTGTTCACAGGGGCCCCAGAGAAAGCTGC 1547

Qy  1249 ATCAAGAGACACGGTCAAGATTGCCAAGGTAACCATGTCCCACAGACGATCTGCC 1308
         ||||||||||||||||||||||||||||||||||||||||||||||
Db  1548 ATCAAGAGCACTGTTAAGATCGCCAAGGTGACCATGTCTGTCTGTTCCACAGACACGTTCTGCC 1607

Qy  1309 GAGGCTCTGTGA 1320
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Db  1608 GAGGCTCTGTGA 1619
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Qy   182 AGAACATCCAGTGTGGGGGAGAACTTCATGAGGACAATAGAGAGTGTTTCATGGTCCTGAACCCCA 241
         |||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 AGAACATCCAGTGTNNNNAGAACTTCATGGACAATAGAGTGTTTCATGGTCCTGAACCCCA 60

Qy   242 GCCAGCAGCTGGGCCATTGCAGTCCTGTCCCTCGTCCCTCAGCGTGGCACCTTCACGGGTCCTGGAGA 301
         ||||||||||||||||||||||||||||||||||||||
Db    61 GCCAGCAGCTGGGCCATTGCAGTCCTGTCCCTCAGCCTGGCACACTTCACGGGTCCTGGAGA 120

Qy   302 ACCTCCTGGTGCTGGTCATCCTCCACTCCCGCAGCCTCCCAGCCCTCAGGCCCTTCCTACC 361
         ||||||||||||||||||||||||||||||||||||||
Db   121 ACCTCCTGGNNNNNNNNGTCATCCTCCACTCCCACTCCCCAGCCCTGCAGGCCTTCCTACC 180

Qy   362 ACTTCATCGGCAGCCTCGGCGGGTGGCAGACCCTCCTCCTGGGGAGGTGTCATTTTTGTCTACAGCT 421
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Db          ...
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RESULT 5
DN533141

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LOCUS       DN533141               769 bp    mRNA    linear   EST 11-MAR-2005
DEFINITION  1361255 MARC 7BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   DN533141
VERSION     DN533141.1  GI:60981254
KEYWORDS    EST.
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 769)
  AUTHORS   Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
            Wray,J.E. and Keele,J.W.
  TITLE     A second set of bovine ESTs from pooled-tissue normalized libraries
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Plate: RLK8056  row: D  column: 11
            Seq primer: GTAATACGACTCACTATAGGG.
            Single pass sequencing. Bases called with phred v0.020425.c and
            trimmed with the aid of the trim_alt option. Vector identified with
            cross_match vo.990329.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /tissue_type="pooled"
                     /clone_lib="MARC 7BOV"
                     /lab_host="DH10B"
                     /clone="MARC 7BOV"
                     /note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
                     Library made with RNA pooled from multiple tissues
                     including ovary, hindbrain, uterus, and day-30 whole
                     embryos."
ORIGIN
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Query Match      48.5%;  Score 639.8;  DB 9;  Length 769;
Best Local Similarity   91.6%;  Pred. No. 9.1e-156;
Matches  677;  Conservative  0;  Mismatches  62;  Indels  0;  Gaps  0;
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Alignment (Qy = query, Db = database sequence):

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Qy  247 CAGCTGGGCCATTGCAGTCCGTCGTCCCTCGACGCTGGGCACGTTCACGGGTCCTGGAGAACTTC 306
Db    1 CAGCTGGGCCATTGCCTGCTGTGGTCTGCCCTCGACGCTGGGCACGTTCACGGGTCCTGGAGAACTG 60

Qy  307 CTGGTGCTGTGGGTCATCCTCCACTCCCGCCAGCCTCCGGCTCGCAGGGCCTTCCTACCACTTC 366
Db   61 CTGGTGCTGTGGGTCATCCTCCACTCCCGCCAGCCTCCGGCTCGCAGGGCCTTCCTACCACTTC 120

Qy  367 ATCGGGCCAGCCTGGCGTGGCGTGGCAGACCCTCTCGGGGAGTGGTGTCATTTTGTCTCACTTCATT 426
Db  121 ATCGGCCAGCCTGGCAGTCGCCGATCTCCTGGGGAGGCGTCATCTTTGTCTATAGCTTCGTC 180

Qy  427 GACTTCCACGTGTTCCACCGCAAAGATAGCCCGAACGTGTTTCTGTTCAAAAACTGGGGTGGG 486
Db  181 GACTTCCACGTGTTCCACCGCAAAGATAGCCCGAACCGTGTTTCTGTTCGTTCAAACTGG 240

Qy  487 GTCACGGGCCTCCTTCACTCCGTCCGGTGGGGCAGCCGCCTGTTCCTCACAGACCAGCAGGTAC 546
Db  241 GTCACGGCCTCGTTCACACAGGCCCCTGGGCCTATAAGAGGATTGTCACCAGGCCCCAGGTAC 300

Qy  547 ATATCCATTCACAGGGCCCCTGGGCTTCTATAAGAGGACATTGTCAGCAGATTCAAGGCCTTTC 606
Db  301 ATATCGATTCACAGGACCCCTGGGCCTATAAGAGGATTCGTCACACGGCCCTGGTG 360

Qy  607 GCGTTTTGGCCTGATTGGTGGACCATAGCCCATTGTGATCGGCCGGTTGCTGCCTCCTCCTGG 666
Db  361 GCGTTTTGGCCTGATTGGTGGACCATCGCAGTTGTGATCGGCCGGTTGCTGCCTCCTCCTGGG 420

Qy  667 AACTGCGGAGAAACTGCAATCTGTTTGCTCGAGACATTTTCCCACACATTGATGAAACCTAC 726
Db  421 AACTGCAAGAAACTGCAATCCGTGTGCTCAGACATTTTCCCTCTCATTGACGAGACCTAC 480

Qy  727 CTGATGTTCTGATCGATCGGGGGTCACCAGCCTACTGCTTCTCGTTCATCGTGTATGGGTACATG 786
Db  481 CTGATGTTCTGGATCGGGGGTCACCAGCCTGGTGCTGTTGCTCGTTCATCGGGTATGCCTACATG 540

Qy  787 TATATTCTTCTGGAAGGCTCCACGCACCGCCATGACCGGCGGCACCCAGGAG 846
Db  541 TACAATCCTTCTGGAAGGCCCACCACCATCCTGTCCGCATGAATCCAGCGTGGTACCCAGAAG 600

Qy  847 AGCATCATCATCCACACGTCTGAGGATAGGGAGAGGGTACACAGTGACCGGCCAGACCAGCC 906
Db  601 AGCATCATCATCCACACCTCCGAGGATGGCAAGGTGACACGGCCGGACCAAGCC 660

Qy  907 CGCATGGACATTAGGTTAGCCAAGAACCCCTGGTCTCGTGGTTTGGTGTTGATCATCTCGC 966
Db  661 CGCATGGACATTCGGCTGGCCAAGAACCCCTGGTCTCGTTGATCATCTGC 720

Qy  967 TGGGGGCCCTCTGCTTGCAA 985
Db  721 TGGGGCCCTCTGCTTCGCAA 739
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RESULT 6
CA327850

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LOCUS       CA327850               752 bp    mRNA    linear   EST 09-JUL-2003
DEFINITION  UI-M-FY0-ccw-f-15-0-UI.r1 NIH_BMAP_FY0 Mus musculus cDNA clone
```

ACCESSION   IMAGE:6825328 5', mRNA sequence.
VERSION   CA327850
KEYWORDS   CA327850.1 GI:24545948
            EST.
SOURCE   Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 752)
  AUTHORS   NIH-MGC http://mgc.ncl.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jim Lin, University of Iowa
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
FEATURES   Location/Qualifiers
     source   1..752
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:6825328"
                     /tissue_type="whole brain"
                     /dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
                     /note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
                     Site_2: Not I; The library was constructed according to
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. Denatured RNA was size fractionated on a 1% agarose
                     gel. First strand cDNA synthesis was primed with oligo-dT
                     primer containing a Not I site. Double strand cDNA was
                     size selected according to mRNA size fraction, ligated
                     with EcoR I adaptor, digested with NotI and then cloned
                     directionally into pYX-Asc vector. The library tag
                     sequence located between the Not I site and the polyA tail
                     is AGGAGACAG. This library was created for the University
                     Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
                     Developing Mouse Nervous System', supported by National
                     Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                     program coordinator."
                     /lab_host="DH10B (T1 phage resistant)"
                     /clone_lib="NIH BMAP_FY0"
ORIGIN
        Seq primer: pYX-5.

        Query Match   48.0%; Score 634.2; DB 4; Length 752;
        Best Local Similarity   90.2%; Pred. No. 2.6e-154;
        Matches 678; Conservative   0; Mismatches 74; Indels   0; Gaps   0;

Qy   394 CTGGGGAGTGTCATTTTTGTTCTACACGCTTCATTCGACTTCCACGTGTTCCACGCAAAGAT 453
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Db   1 CTGGGAAGTGTCATCTTTGTCTCACAGCTTGTTGACTTCCACGTGTTCCACCGCAAAGAT 60

Qy   454 AGCCGGCAAGCGTGTTTCTGTTCAAACTGGGTGGGGGTCACGGGCCTCCTTCCACTGCCTTCCGTG 513
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Db   61 AGTCCCAATGGTGTTTCTGTTCAAACTGGGGGGGTTACCGGCCTCCTTCCACTGCCATCCTG 120

Qy   514 GGCAGCCTGTGTTCCTCACAGCCATCGACAGGTACATATCCACACAGCCCCTGGCCTAT 573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 GGCAGCCTGTTCCTCACGGCCCATCGACAGCACAGGTACATATCCACATTCACAGGCCCTAT 180

Qy   574 AAGAGAGATTGTCACCAGGCCCAAGGCCGTGGTTAGCGTTTTTCCCTGATGTGAGTGGACTATTAGCC 633
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   181 AAGAGGAATCGTCACCAGGCCCAAGGCCGTAGTGGGGCCCTTTGCTTGATGTGGACTATTGCA 240

RESULT 7
LOCUS   CA328435   737 bp   mRNA   linear   EST 09-JUL-2003
DEFINITION UI-M-FY0-cdb-f-10-0-UI.r1 NIH_BMAP_FY0 Mus musculus cDNA clone
            IMAGE:6827243 5', mRNA sequence.
ACCESSION   CA328435
VERSION   CA328435.1 GI:24545633
KEYWORDS   EST.
SOURCE   Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 737)
  AUTHORS   NIH-MGC http://mgc.ncl.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jim Lin, University of Iowa
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
FEATURES   Location/Qualifiers
     source   1..737
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:6827243"

Seq primer: pYX-5.

Qy   634 ATTGTGGATCGGCGTGCCTCCTCCTGGGGTGGGGTGGGTGACATGGCGAGGAAACTGCAATCTGTTGC 693
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Db   241 ATAGTAAATGCTGTGTGTTGCCTCTCCTGGGGTCGGTGGGTGGAACTGCAAGAGCTGCAATCTGTTTGC 300

Qy   694 TCAGACATTTTCCACACATTGATGAAAACTACCTGATGTTGTTCTGGATCGGCGGGTCACCAGC 753
              |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 TCAGACATCTTCCCACTCATTGATGAAAACTACCTTAGTTCTGGATCGGCGGGGTCACCAGT 360

Qy   814 GCCGTCCGCATGATTCAGCGTGGCACCCAGAAGAGCATCATCATCCACACAGGTCTGAGAT 873
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 GTGCTGTTGCTGTTCATTGTATGCATACAATGTACATTCTCTGCGAAAGGCCAC 420

Qy   814 GCCGTCCGCATGATTCAGCGTGGCACCCAGAAGAGCATCATCATCCACACAGGTCTGAGAT 873
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GCAGTTCGGCATGATCCAGCGTGGAAACCCAGAAAAGCATCATCACACCTCAGAAGAT 480

Qy   874 GGGAAGGTACAGGGTGACCCGGCCAGACCAAGCCCGCGCCATGGACAATTAGGTTGCAAGACC 933
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 GGCAAGGTGCAGGTGACACGGGCCGCATGGACAATTAGGCTGGCCCAAAACC 540

Qy   934 CTGGTCCTGATCCTGGTGCTGTGTTGATCAATCTGCGGGGCCCTCGGCTTGCAATCATGGTG 993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 CTGGTTCTGATCCTGGTGGTGTTGATCAATCTGCGTGGGGGCCCTCGCTTGCGATCATGGTG 600

Qy   994 TATGATGTCTTGGGAAGAGATGAACAAGCTCATTAAGACGGGTTGCATTCTGCAGTATG 1053
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Db   601 TATGATGTCTTTGGGAGATGAACAAGCTTATCAGAACGGTGTTTGCCTTCTGTAGTGTATG 660

Qy   1054 CTCTCGCCCTGCTGAACTCCACCGTGAAACCCCATCATCTATGCTTCTGAGGAGTAAGGACTG 1113
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CTCTGCCCTGCTGAACTCCACCGNTGAAACCCCATCATCTATGCTCTGAGGAGACAAGGACTG 720

Qy   1114 CGACACGGCTTTCCGGAGCATGTTTCCCCTCTG 1145
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Db   721 AGACACGCTTTCCGGCAGCATGTTCCCCTTCATG 752

/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH BMAP FY0"
/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGGAGACAG. This library was created for the Univerity
Iowa Brain Anatomy Project (BMAP); 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

ORIGIN
Query Match   Best Local Similarity   90.9%;   Pred. No. 2.6e-153;
Matches 670; Conservative   0;   Mismatches   67; Indels   0;   Gaps   0;

Qy   414 CTACAGCTTCATTGACTTCCACGTGTTCCACACCGCCAAAGATAGCCGCAAGCGTGTTTCTGTT   473
Db   1 CTACAGCTTGTTGACTTCCACGTGTTCCACACCGCCAAAGATAGTCCCAAATGTGTTTCTGTT   60
Qy   474 CAAACTGGGTGGGGTCACGGCCCTCCTTCACTGCCTCCGTGGGCCAGCCTGTTCCTCACGC   533
Db   61 CAAACTGGGTGGGGTTACCGCCTCCTTCACTGCCTCCGTGGGCCAGCCTGTTCCTCACGGC   120
Qy   534 CATCGACAGGTACATATCCATTCACAGCCCCCTGGGCTTATAAGAGGATTGTCACCAGGCC   593
Db   121 CATCGACAGGTACATATCCATTCACAGCCCTCGGCCTTATAAGAGGATCGTCACCAGGCC   180
Qy   594 CAAGGGCCGTGGTAGGCGTTTTGCCTGATGTGGACCATAGCCAATTGTGTAGGCGTGCTGCC   653
Db   181 CAAGGGCCGTAGTGGCCTTTTGCTGAGTGGACTATATTGCTCAATAAGTAATTGCTGTGTTTGCC   240
Qy   654 TCTCCTGGGCTGGAACTGCGAGAAACTGCAATCTGTTGTTCCTCAGACACATTTTCCCACACAT   713
Db   241 TCTCCTGGGCTGGAACTGCAATCTGTTGTTGCTCAGACATCTTCCCACTCAT   300
Qy   714 TGATGAAAACCTACCTGATGTGTTCTGGATCGGGGTCACGCAGGGTACTGCTTCTCTTCACGT   773
Db   301 TGATGAAAACCTACCTNATGTTCTGGATCGGGGTCACGCAGGGTACTGCTCTGTTGCATTGT   360
Qy   774 GTATGCTACACGTGTATAATTCTCTGGAAGGGCTCACCAGCCAACGCCGTCCGCCATGATTCAGCG   833
Db   361 GTATGCATACACGTACATTCTCTGGAAGGGCTCACAGCCCACGGTGCCGCCATCGATCCAGCG   420
Qy   834 TGGCACCCAGAAGAAGCATCATCACACGTCTGAGGATGGGAAGGTACAGGTGACCCG   893
Db   421 TGGAACCCAGAAAAGCATCATCACACTCACGGGAGAATGCCAAGGTGCAGGTGACACG   480
Qy   954 GTTGATCATCTTCGCTGCGGGCCCTCTGCTTGCAATCATGGGTGATGATGATCTTCTTTGGGAAGAT 1013
Db   481 GCCTGACCTCAAGCCCGCATGGAACAATTAGGCTGGCGCCCAAAACCCTGGTTCTGATCCTGGTGGT   540
Qy   894 GCCAGACCAAGCCCGCATGGACATTAGGTTAGCCAAGAACCTGGTCGTCCTGGATCCTGGGTGGT   953
Db   541 GTTTGATCATCTCTGCGGGCCCTCTGCTTGCAATCATGGGTGATGATGTTCTTTGGGAAGAT   600
Qy   1014 GAACAAGCTCATTAAGACGGTGTTGCATTCTGCAGTATGCTGCTGCTGAACTCCAC 1073
Db   601 GAACAAGCTTATCAAGACGGGTGTTTGCCTTCTTGCTGTAGTGCTGAACTCCAC   660
Qy   1074 CGTGAACCCCATCATCATCTATGCTCTGAAGGAGGTAAGGAACCTGACACCGCTTTCCGGACGAT 1133
Db   661 CGTGAACCCCATCATCTATGCTCTGGGGAGCAAGGAACCTGAGACATGCTTTCCGGCAGCGAT   720

RESULT 8
Qy   1134 GTTTCCCTTCATGTGAAG 1150
Db   721 GTTCCCTTCATGTGAAG   737

DY320503
LOCUS   DY320503
DEFINITION AGENCOURT_66892761 NIH MGC_365 Rattus norvegicus cDNA clone
            IMAGE:8362287 5', mRNA sequence.
ACCESSION   DY320503
VERSION   DY320503.1   GI:87003257
KEYWORDS   EST.
SOURCE   Rattus norvegicus (Norway rat)
ORGANISM   Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1 (bases 1 to 717)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg, 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Howard J. Jacob
            cDNA Library Preparation: Express Genomics
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            http://image.llnl.gov/.
            Plate: LLAM18153 row: n column: 13
            High quality sequence stop: 648.
FEATURES   Location/Qualifiers
source   1..717
                /organism="Rattus norvegicus"
                /mol_type="mRNA"
                /db_xref="taxon:10116"
                /clone="IMAGE:8362287"
                /tissue_type="whole brain, pool of 7"
                /clone_lib="NIH MGC 365"
                /lab_host="DH10B TonA"
                /note="Organ: brain/CNS; Vector: pExpress-1; Site 1:
                EcoRV; Site 2: NotI; cDNA was primed using oligo-dT
                primer: 5'-PGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)25-3' and
                cloned into the EcoRV/NotI sites of pExpress-1.
                Size-selection >1.3kb resulted in an average insert size
                of 2.0kb. This is a non-normalized primary library
                (normalized primary library is NIH MGC 366) and was
                constructed by Express Genomics (Frederick, MD) for the
                Mammalian Gene Collection http://mgc.nci.nih.gov/."

ORIGIN
Query Match   Best Local Similarity   91.2%;   Pred. No. 1.3e-149;
Matches 654; Conservative   0;   Mismatches   63; Indels   0;   Gaps   0;

Qy   463 GTGTTTCTGTTCAAAACTGGGGTGGGGGTCACGGCGCTCCTTCACTGCCTCCGTGGGCCAGCCTG   522
Db   1 GTGTTTCTGTTCAAACTGGGGGGTTACCAGCCTCCTTCACTGCCTTCTGTGGGCCAGCCTG   60
Qy   523 TTCCTCACGACCATCGACAGCATCGACAGGTACATATCCATTCACAGCCCCTGGCTTATAAGAGGATT   582
Db   61 TTCCTCACGACCATCGACAGGTACATATCCATTCACAGCCCTCGGCCTTATAAGAGGATC   120
Qy   583 GTCACCAGGCCCAAGGCCGTGGTAGGCGTTTTGCCTGATGTGGACCATAGCCATTGTGATC   642
Db   121 GTCACCAGGCCCAAGGCCGTTGTGGCCTTTTGCTGAGTGGACTATATCGGCAATAAGTAATC   180
Qy   643 GCCGTGCTGCCTCTCCTGGGCTGGAACTGCGAGAAACTGCAATCTGTTTGCTCAGACATT   702

```
RESULT 9
LOCUS       CB244710               844 bp    mRNA    linear   EST 09-JUL-2003
DEFINITION  UI-M-FY0-cdr-m-10-0-UI.r1 NIH_BMAP_FY0 Mus musculus cDNA clone
            IMAGE:6833555 5', mRNA sequence.
ACCESSION   CB244710
VERSION     CB244710.1  GI:28366354
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 844)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jim Lin, University of Iowa
            cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
            Seq primer: pYX-5.
FEATURES             Location/Qualifiers
     source          1..844
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:6833555"
                     /tissue_type="whole brain"
                     /dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
                     /lab_host="DH10B (T1 phage resistant)"
                     /clone_lib="NIH_BMAP_FY0"
                     /note="Organ: Brain; Vector: pYX- Asc; Site 1: EcoR I;
                     Site 2: Not I; The library was constructed according to
                     BonaIdo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. Denatured RNA was size fractionated on a 1% agarose
                     gel. First strand cDNA synthesis was primed with oligo-dT
                     primer containing a Not I site. Double strand cDNA was
                     size selected according to mRNA size fraction, ligated
                     with EcoR I adaptor, digested with NotI and then cloned
                     directionally into pYX-Asc vector. The library tag
                     sequence located between the Not I site and the polyA tail
                     is AGCGAGACAG. This library was created for the University
                     Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
                     Developing Mouse Nervous System', supported by National
                     Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                     program coordinator."
ORIGIN

Query Match
Best Local Similarity   45.7%;   Score 602.8; DB 4;   Length 844;
Best Match              90.6%;   Pred. No. 4.4e-146;
Matches  665;  Conservative  0;  Mismatches  67;  Indels  2;  Gaps  2;
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Qy 285 CTTCACGGTCCTGGAGGAACCTCCTGGTGCTGCTGGGGTCATCCTCCCGGCAGCCTCCG 344
Db   1 CTTCACGGTTCTGGAGGAACCTCCTGGTGCTGCTGGGGTCATCCTCCCGGCAGCCTCCG 60

Qy 345 CTGCAGGCCTTCCTACCACTTCATCGGCAGCCTGGCCGTTGGCAGAGACCTCCTGGGGAGTGT 404
Db   61 ATGCAGGGCCTTCCTACCACTTCATTGGGACAGCCTGGCCGATCTCCTGGGAAGTGT 120

Qy 405 CATTTTTGTTCACAGCTTCATTGACTTCCACGGTGTTCCACGGCGAAAGATAGCCCGCAACGT 464
Db 121 CATCTTTGTGTCTACAGCTTTGTTGGACTTCCACGGTTCCACGGCGAAAGATAGTCCCAAAGT 180

Qy 465 GTTTCTGTTCAAACTGGGTGGGGTCACGGCGCCTCCTTCACTGCCTCCGGTGGGGCAGCCTGTT 524
Db 181 GTTTCTGTTCAAACTGGGTTTGCCGGTTACCGCCCTCCTTCACAGCATCTGTGGGCAGCCTGTT 240

Qy 525 CCTCACAGCCATCGACACAGGTACATAATCCATTCACACGACCCTCCTTGCCCTATAAGAGGATTGT 584
Db 241 CCTCACGGGCCATCGACACAGGTACATAATCCATTCACAGGCCTCTGGCCCTATAAGAGGATCGT 300

Qy 585 CACCAAGGGCCCAAGGCCGTGGGTACGGTTTTGGCCTGAGTGGGACCATAGGCCATTGTGATCGC 644
Db 301 CACCAAGGGCCCAAGGCCGTAGGTGGCCTTTTGGCCTTGGATGTGGACTATTGCAATAGTAATTGC 360

Qy 645 CGTGCGTGCCCTCCTCTCGGGCGTGGGAACTGCGAGAAACTGCAATCTGTTTGCTCAGACATTT 704
Db 361 TGTGTGTGGCCTCTCCTGGGGCTGGAACTGCAGGAAGCTGCAATCGTTTGCTCAGACATCTT 420

Qy 705 CCCACACATTGATGAAAACCTACCTGATGTTTCGGATGTCGGGTCACCGGGTACTGCTTCT 764
Db 421 CCCACTCATTGATGAAAACCTACCTGATGTTTCGGATCGGATCGGGTCACCGGTGCTGCT 480

Qy 765 GTTCATCGTGTATGGCGTACATGTAATTCTCTGGAAGGCTCACGAGCCACGCGCGTCCGGAT 824
Db 481 GTTCATTCTGTATGCATACATGTTACATTCTCTGGAAGGCTCACAGCCAGCAGCTTCGGAT 540

Qy 825 GATTCAGCGCTGGGCACCCAGAAGAGCATCATCACACGTCTGAGGATGGGGGAAGGTACA 884
Db 541 GATCCAGCGGTGGAACCCAGAAAAGCATCATCATTCACACTCAGAGAGATGGCAAGGTGCA 600

Qy 885 GGTGACCCGGCCAGACCAAGCCCGCARGGACATTAGGTTAGCAACGCACCCTGCTTCCGGAT 944
Db 601 GGTGACACGGGCCTGACCAAGCCCGCATGGAACATGGACATCTGGCTGGCCAA-ACCCTGGATCTGAT 659

Qy 945 CCTGGGTGGTGTTGATCAATCTGCTGGGGGCCCCTCTGTTGCTTGCAATCATGGGTGTATGGGTGGTTGCTT 1004
Db 660 CCTGGGTGGTGTTGATCAATCTGCTGGGG-CCTCTGCTTGGGACATGTGGTTATGATGTGCTT 718

Qy 1005 TGGGAAGATGAACA 1018

Db   719 TGGGAAGGAGAACA 732
      ||||||||||||||

RESULT 10

LOCUS   CF533059
DEFINITION UI-M-FY0-cgs-f-20-0-UI.r1 NIH_BMAP_FY0 Mus musculus cDNA clone
            IMAGE:30361963 5', mRNA sequence.
ACCESSION   CF533059
VERSION   CF533059.1 GI:34585027
KEYWORDS   EST.
SOURCE   Mus musculus (house mouse)
  ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 737)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jim Lin, University of Iowa
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr.M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Distribution Information can be found at
            http://genome.uiowa.edu/distribution/mousef1.html
            This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
            Seq primer: pYX-5.
FEATURES   Location/Qualifiers
     source   1..737
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:30361963"
                     /tissue_type="whole brain"
                     /dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
                     /clone_lib="NIH_BMAP_FY0"
                     /lab_host="DH10B (T1 phage resistant)"
                     /note="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I;
                     Site 2: Not I; The library was constructed according
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. Denatured RNA was size fractionated on a 1% agarose
                     gel. First strand cDNA synthesis was primed with oligo-dT
                     primer containing a Not I site. Double strand cDNA was
                     size selected according to mRNA size fraction. ligated
                     with EcoR I adaptor, digested with NotI and then cloned
                     directionally into pYX-Asc vector. The library tag
                     sequence located between the Not I site and the polyA tail
                     is AGGGAGACAG. This library was created for the University
                     Iowa Brain Anatomy Project (BMAP) 'Gene Discovery in the
                     Developing Mouse Nervous System' supported by National
                     Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                     program coordinator."
ORIGIN

Query Match   45.4%; Score 599.8; DB 5; Length 737;
Best Local Similarity   89.1%; Pred. No. 2.6e-145;
Matches 657; Conservative   0; Mismatches 79; Indels   1; Gaps   1;

Qy   148 AACAAGMGTCTCTCTCCGTCCTTCAAGGAGAATGAGGAGAACATCCAGTGT-GGGGAGAACTT 206
         ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db   1 ACACAAGTCTCTCCATCCGTTCAAGGAGAGAACGAGGAGAACATCCAGTGTNGGGGAGAATTT 60

Qy   207 CATGGACATAGAGAGTGTTTCATGGTCCTGAACCCCAGACCCAGCTGGCCCATTGGCAGTGCT 266
         ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   61 TATGGACATGGAGGTGCTTCATGATTCTGAATCCCAGCCAGCAGCTGGCCCATCGCCCTGTCCT 120

Qy   267 GTCCCTCACGCTGGGCACCTTCACGGTGTCTGGGAGAAACTCCTGGTGCTGCTGTGGCTCATCCT 326
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   267 GTCCCTCACGCTGGGCACCTTCACGGTGTCTGGGAGAAACTCCTGGTGCTGCTGTGGCTCATCCT 326

Db   121 GTCCCTCACCCTGGGCGACTTCACGGTTCTGGGAGAACCTGCTGCTGTATGTGTCATCCT 180

RESULT 11

LOCUS   CO955553/c
DEFINITION AGENCOURT_30842409 NIH_MGC_146 Homo sapiens cDNA clone
            IMAGE:7389731 3', mRNA sequence.
ACCESSION   CO955553
VERSION   CO955553.1 GI:51324126
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 774)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE   National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT   Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Guthrie cDNA Resource Center
            cDNA Library Preparation: Guthrie cDNA Resource Center
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov

Db   721 CAGAGATGGGCAAGGTGC 737

Db   867 TGAGGATGGGAAGGTAC 883
         |||||| |||||||

Qy   721 CAGAGATGGGCAAGGTGC 737

Qy   747 CACCAGCGTACTGCTTCTTCTTGTTCATCGTGTATCGTACATGTAATGTAATTCTCTGGAAGGCTCA 806
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601 CACCAGCGTGCTGCTTGCTGTTCATTGTTGTATCGTACATGTAATGTAATTCTCTGGAAGGCTCA 660

Qy   601 CACCAGCGTGCTGCTTGCTGTTCATTGTTGTATCGTACATGTAATGTAATTCTCTGGAAGGCTCA 660

Qy   807 CAGGCACCGCCGTCCGCATGAATTCAGCCTGGCCGACCCAGGAGGGCATCATCATCCACACGTC 866
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   661 CAGCCACCGCAGTTCGCATGATCCAGCCTGGGACCCAGGAGGGCATCATCATCATCACANCT 720

Qy   687 TGTTTGCTCAGACATTTTCCCACACATTGATGAAAAACTACACCTGATGGTTGCTTTCTGGATCGGGGT 746
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 TATTGCAATAGTAATTGCTGGTTGTGTTGCCTCTTCCTCTGGCGCTGGGGACCTGCAAGAAGCTGCAATC 540

Qy   481 TATTGCAATAGTAATTGCTGGTTGTGTTGCCTCTTCCTCTGGCGCTGGGGACCTGCAAGAAGCTGCAATC 540

Qy   567 GGGCCTATAAGAGGAGATTGTCACCAGGCGCCCAAGCCGGTGGTAGGCGTTGGTTTTGCCTGATGTGGAC 626
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 GGGCCTATAAGAGGAGATCGTCACCAGGCGCCCAAGCCGTGAGTGGCCTTTTGCCTGATGTGGAC 480

Qy   421 GGGCCTATAAGAGGAGATCGTCACCAGGCGCCCAAGCCGTGAGTGGCCTTTTGCCTGATGTGGAC 480

Qy   507 CTCCGTGGGGCACCGTGTTCCTCACAGCCGCCATCACAGCGTACACATTCACAGAGCCCCT 566
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 AGCTGTGGGCAGGCCTGTTCCTCACGGCGCCATCAGACAGGTTACATATCACACAGGCCCTCT 420

Qy   361 AGCTGTGGGCAGGCCTGTTCCTCACGGCGCCATCAGACAGGTTACATATCACACAGGCCCTCT 420

Qy   447 CAAAGATAGCCGCAACGGTGTTTCTGTTCATCCTGTTCAAACTGGGTGTGGGGTTCACGGGCGCCTTCTTCACTGC 506
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CAAAGATAGTCCCAATGTGTTTCTGTTCAAACTGGGTTACCGCCTCCTTCACAGC 360

Qy   301 CAAAGATAGTCCCAATGTGTTTCTGTTCAAACTGGGTTACCGCCTCCTTCACAGC 360

Qy   387 AGAACCTCCTGGGAGTGGTCGCATTTTTGCTACAGCTTCAGCTTCACGTGTTCCACG 446
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 CGATCCTCTGGGAAGTGTCATCTTTGTCTACAGCTTCTACTGACTTCACGTTGCACG 300

Qy   241 CGATCCTCTGGGAAGTGTCATCTTTGTCTACAGCTTCTACTGACTTCACGTTGCACG 300

Qy   327 CCATCTCCGCCACCTTCCGCTGCGACTTCCTTCCTTACCACTTCATCCAGGGTGGGC 386
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 TCACTCCCGCCAGTCTCCGGATGGCAGGCCCTTCCTACCACTTCATCGGAGAACCTGCTGGC 240

Qy   181 TCACTCCCGCCAGTCTCCGGATGGCAGGCCCTTCCTACCACTTCATCGGAGAACCTGCTGGC 240

Qy   121 GTCCCTCACCCTGGGCGACTTCACGGTTCTGGGAGAACCTGCTGCTGTATGTGTCATCCT 180

RESULT 12

First section:

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Plate: IRB17  row: e  column: 09
High quality sequence start: 125
High quality sequence stop: 607.
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FEATURES   Location/Qualifiers
  source   1..774
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                   /mol_type="mRNA"
                   /clone_lib="IMAGE:7389731"
                   /db_xref="taxon:9606"
                   /clone="IMAGE:7389731"
                   /tissue_type="mixed"
                   /lab_host="DH10B (T1-phage-resistant)"
                   /clone_lib="NIH_MGC_146"
                   /note="Vector: pcDNA3.1; Site 1: multiple; Site 2:
                   multiple; ORF's were PCR-amplified (from IMAGE clones or
                   from commercially available cDNA libraries) and cloned by
                   the Guthrie cDNA Resource Center (www.guthrie.org/cDNA)
                   into pcDNA3.1. For specific information on cloning sites
                   (which vary by clone), please refer to the Guthrie
                   website, using the Guthrie ID given in the file
                   ftp://image.llnl.gov.image.rearrayed_plates/IRSF.presv.dat
                   a. Note: this is a NIH_MGC library."

ORIGIN

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Query Match        44.9%;  Score 592.2;  DB 8;  Length 774;
Best Local Similarity  99.0%;  Pred. No. 2.6e-143;
Matches  616;  Conservative  0;  Mismatches  4;  Indels  2;  Gaps  2;
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Qy    690 TTGCTCAGACATTTTCCCACACAATTGATGAAAACTACCTGATGTTCTGGATCGGGGTCAC 749
          |||||||||||||||||||||||| |||||| ||||||| | |||||||||||||||||||
Db    643 TTGTTCAGACATTTTCCCACACATT-ATGAAAACNTACCTGATG--TCTGGATCGGGGTCAC 586

Qy    750 CAGGGTACTGCTTCTCGTTCATCGTGTATCCGTACATGTATAATTCTTCTGGAAGGCTCACAG 809
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    585 CAGGGTACTGCTTCTCGTTCATCGTGTATGCGTACATGTATAATTCTTCTGGAAGGCTCACAG 526

Qy    810 CCACGCCGTCCGCATGATTCAGCGTGGCACCCAGAAGAGCCATCATCATCCACACGTCTCGA 869
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    525 CCACGCCGTCCGCATGATTCAGCGTGGCACCCAGAAGAGCCATCATCATCCACACGTCTCGA 466

Qy    870 GGATGGGAAGGGTACAGGTGACCCGGCCCAGACCAACAGCCATTAGGTTAGCCAA 929
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    465 GGATGGGAAGGGTACAGGTGACCCGGCCCAGACCAACAGCATTAGGTTAGCCAA 406

Qy    930 GACCCTGGCTCCTGAATCCTGGTGGTGTGTTGATCATCTGCTGGGGCCCTTGCAAATCAT 989
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Db    525 CCACGCGCTCCGCATGATTCAGCGTGGCACCCAGAAGAGCCATCATCATCCACACGTCTCGA 466

Qy    990 GGTGTATGATGTCTTTGGGAAGATGAACAAGCTCATTAAGACCAGTGTTGCATTCTGCAG 1049
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    345 GGTGTATGATGTCTTTGGGAAGATGAACAAGCTCATTAAGACCAGTGTTGCATTCTGCAG 286

Qy   1050 TATGCTCTGCCTGCTGAACTCACCGTGAAACCCATCATCTATGCTCTGAGAGGAGTAAGGA 1109
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    285 TATGCTCTGCCTGCTGAACTCACCGTGAAACCCATCATCTATGCTCTGAGAGGAGTAAGGA 226

Qy   1110 CCTGCGACACGCTTTCCGGAGCAGTGTTCCCTCTTCCTTGTGAAGGCAGGCAGCCTCTGGA 1169
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    225 CCTGCGACACGCTTTCCGGAGCAGTGTTCCCTCTTCCTTGTGAAGGCAGGCAGCCTCTGGA 166

Qy   1170 TAACAGCATGGGGGACTCGGACTGCACCAAAACACCGCAAGTGTTGCAGTGTTCA 1229
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    165 TAACAGCATGGGGGACTCGGACTGCACAAAACACGGCAAGTGTTGCAGTGTTCA 106

Qy   1230 CAGGGGCCGCAGAAAAGCTGCATCAAGAGGACACGGTCACATCAAGAGTTAACCATGTCTGT 1289
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    105 CAGGGGCCCCAGAAAAGCTGCATCAAGAGGACACGGTCAAGAGTTAACCATGTCTGT 46

Qy   1290 GTCCACAGACACGCTCTGCCGAG 1311
          ||||||||||| |||||||||||
Db     45 GTCCACAGACACTTCTCGCCGGG 24
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Second section:

```
CC202312/c

LOCUS       CC202312              1151 bp    DNA     linear   GSS 09-MAY-2003
DEFINITION  CH261-70E11_Sp6.1 CH261 Gallus gallus genomic clone CH261-70E11,
            genomic survey sequence.
ACCESSION   CC202312
VERSION     CC202312.1  GI:30482109
KEYWORDS    GSS.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 1151)
  AUTHORS   Kremitzki,C., Higginbotham,J., Wylie,K., Carter,J., McPherson,J.,
            Warren,W., Graves,T., Mardis,E. and Wilson,R.
  TITLE     Gallus gallus BAC End Reads
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Richard K. Wilson
            Genome Sequencing Center
            Washington University School of Medicine
            Email: submissions@watson.wustl.edu
            /cell_line="UCD001, inbred 256"
            /clone_lib="CH261"
            Insert Length: 182000   Std Error: 0.00
            Seq primer: Sp6 ATTTAGGTGACACTATAG
            Class: BAC ends
            /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
            CH261 Female chicken library - for library and clone
            ordering information: http://www.chori.org/bacpac"
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FEATURES   Location/Qualifiers
  source   1..1151
                   /organism="Gallus gallus"
                   /mol_type="genomic DNA"
                   /strain="Red Jungle Fowl"
                   /db_xref="taxon:9031"
                   /clone="CH261-70E11"
                   /sex="female"
                   /clone_lib="CH261"
                   High quality sequence start: 39
                   High quality sequence stop: 737.

ORIGIN

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Query Match        44.9%;  Score 592.2;  DB 12;  Length 1151;
Best Local Similarity  79.3%;  Pred. No. 2.9e-143;
Matches  727;  Conservative  0;  Mismatches  188;  Indels  2;  Gaps  2;
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Qy    128 TGAACATTACAGAATTTTACAACAAGTCTCTCTCGTCCTTCACAAGG-AGAATGAGGAGAAC 186
          ||||||||||||||||  || |||||||||||||||||||||  ||||  ||||||||||||
Db    949 TCAATATCACAGAGTTTTCACAAAAATCCTTGTTCCCGTTTAAGGAAAAATGGGGAGGAGACC 890

Qy    187 ATCCAGTGTGGGAGGAGAACTTCATGGACACATAGAGTGTTGTTCCCTGAACCCCAGCCAG 246
          |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db    889 ATACAGTGTGGGAGGAGAACTTCATGGAGTATAGGATGTTTTATGAATCTAAAAATCCCAGCCAG 830

Qy    247 CAGCTGGCCATTGCAGTCCTGTTCCCTCA-CGCTGGGCACCTTCACGGTCCTGGAACCT 305
          ||||||||||||||||||||||||||||  |||||||||||||||||||||||||||||
Db    709 CAGCTGGCCATTGCAGTCCTGTTGTCCCTCACGCTGGGCACCTTCACGGTCCTGGAACCT 650

Qy    306 CCTGGGTGCTGTGCGTCATCCTCCACTCCCGCCAGCCTCCGCTGCAGGCCGCTTCCTACCACTT 365
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    769 CCTGGTCCTGTGGTGGTTATCCTCCACTCCCGGAAGCCTGCGGAACCCTCCTTTATCATTT 710

Qy    426 TGACTTCCACGGTGTTCCACCCGAAAAGATAGGGCCGGCAACGTGTTTTCTGTTTCAAAACTGGGTGG 485
          ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db    649 TGATTCCATGTTTTTCACCGAAGGACAGCCCCAACGTCTTGTTCTGTTTCAAAGTGGGTGG 590

Qy    306 CCTGGGTGCTGTGCGTCATCCTCCACTCCCGCCAGCCTCCGCTGCAGGCCGCTTCCTACCACTT 365
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    649 TGATTCCATGTTTTTCACCGAAGGACAGCCCCAACGTCTTGTTCTGTTTCAAAGTGGGTGG 590

Qy    486 GGTCACGGCCGCCTCCTTCACTGCCTCCCGTGGGCGCAGGCCTGCGGTCCTGCAGCGCCATCGACACAGGTA 545
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Qy    589 AGTTACAGCGCTCCTTCACCGGCCTCCGTAGGTAGCCCTTTTTCTCACGGGCCAATAGACCGGTA 530
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RESULT 13
DN515498/c

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LOCUS       DN515498                 680 bp    mRNA    linear   EST 10-MAR-2005
DEFINITION  1252753 MARC 7BOV Bos taurus cDNA 3', mRNA sequence.
ACCESSION   DN515498
VERSION     DN515498.1  GI:60725688
KEYWORDS    EST.
SOURCE      Bos taurus (cattle)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 680)
  AUTHORS   Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
            Wray,J.E. and Keele,J.W.
  TITLE     A second set of bovine ESTs from pooled-tissue normalized libraries
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called with phred v0.020425.c and
            trimmed with the aid of the trim_alt option. Vector identified with
            cross_match v0.990329.
            Plate: RLK8030  row: L  column: 20
            Seq primer: TAGAAGGACAGTCGAGG.
FEATURES             Location/Qualifiers
     source          1..680
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                     /clone_lib="MARC 7BOV"
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ORIGIN

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Query Match            43.8%;  Score 577.6;  DB 9;  Length 680;
Best Local Similarity  90.6%;  Pred. No. 1.6e-139;
Matches  616;  Conservative  0;  Mismatches  64;  Indels  0;  Gaps  0;

Qy   224  TCATGGTCCTGAACCCCAGCCAGCACCAGCGTGGCCATTGGCAGTCCTGGTCCCTGGGCCA  283
Db   680  TCATGATCCTGAACCCCAGCCAGCACCAGCGTGGCCATCGGCTGTCCTTCCCTCACGTTGGGCA  621

Qy   284  CCTTCACCGGTCCTGGAGAACCCTCCTGGTGCTGTGTGGTGGTCATCCTTCCCACTCCGGAGCCTCC  343
Db   620  CCTTCACGGTCCTGGAGAACCTGCCTGGTGCTCGTGGTGGTCATCCTTCCCATTCCGCGAGCCTCC  561

Qy   344  GCTGCAGCGCCCTTCCTCACCTCACTTCATCCGGCAGCGCCTGGGGGTGGCAGACCTGCTTGGGGAGTG  403
Db   560  GCTGCCGCGGCCCTCTTACCCACTTCATCCGGCAGCCGCCAGTCGGGGGTGGCAGACCTGCTTCCTGGGAGCCG  501

Qy   404  TCATTTTTGTCTACAGCTTCATTGACTTCACAGTCGTTCCAGGTGGTTCCACCGGCAAAGATAGGCGCAACG  463
Db   500  TCATCTTCGTCTATAGCTTCGTCGACTTCCAGGTGGTTCCACCGGCAAAGACACAGCCCCAACG  441

Qy   464  TGTTTCTGTTCAAAACTGGGGTGGGGTCAGGGGTCAGCCTCCTTCACTGCCTCCGTGGGGCAGCCTGT  523
Db   440  TGTTTCTGTTCAAAACTGGGGTCAGGGGTCACGGGCCTCGGTGTCACAGCCTCGGTGGGCAGCCTGT  381

Qy   524  TCCTCACAGCCATCGACAGGTACATATCCATTCACACAGGCCCTGGCCTTATAGAGGAGGATTG  583
Db   380  TCCTCACCGGCCATCGACACGGTACATATCGATTCACAGGCCCTGGCCTTATAAGAGGATCG  321

Qy   584  TCACCAGGCCCAAGGCCCGTGGTAGCGTTTTGCCTGATGTGGACCATAGCCATTGTTGATCG  643
Db   320  TCACACGGCCCTAAGGCCCGTTGGTGGCGTTTTGCCTGATGTGGACCATTGGCGATTGTTGATCG  261

Qy   644  CCGTGCTGCCCTCTCCCTGGGGCTGGAGAAACTGCGAGAAACTGCAATCTGTTTGCTCAGACATTT  703
Db   260  CCGTGCTTGCCCCCCTGCCTAGGCTGGGAACTGCAAAGAAACTGCAATCGGTGTGCTCAGACATTT  201

Qy   704  TCCCACACATTGATGAAACCTACCTGAGTTCTGGATCGGGTCACCGGCTCTC  763
Db   200  TCCCTCTCATCGACGAGACCTACCTGAGTGTTCTGGATCGGGGTCACCGGCTGCC  141

Qy   764  TGTTCATCGGTGTATGCGGTACATGTATAATTCTCTGGGAAGGCTCACGCCCACGCCGTCCGA  823
Db   140  TGTTCATCGGTGTAAGCGGTACATCCCTCTGGGAAGGCGACACAGCCACATGCTGTCCCGA  81

Qy   824  TGATTCAGGGTGGCGCACCCAGGAAGGCATCATCATCCACACCACGTGTTGAGGATGGGAAGGTAC  883
Db    80  TGATCCAGCGTGGTACCCAGGAAGAGCATCATCATCCACACGTCCGAGGATGGCAAGGTGC  21

Qy   884  AGGTGACACCCGGCCCAGACCAA  903
Db    20  AGGTGACACGGCCCGAAAAA  1
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RESULT 14
BU705501

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LOCUS       BU705501                 780 bp    mRNA    linear   EST 15-JUL-2003
DEFINITION  UI-M-FO0-cac-a-11-0-UI.r1 NIH_BMAP_FO0 Mus musculus cDNA clone
            IMAGE:6409234 5', mRNA sequence.
ACCESSION   BU705501
VERSION     BU705501.1  GI:23635044
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 780)
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/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
library made with RNA pooled from multiple tissues
including ovary, hindbrain, uterus, and day-30 whole
embryos."

RESULT 13 alignment (left column):

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Qy   546  CATATCCCATTCACAGGCCCTGGCCTTGGCCTTATAGAGGATGTCACCAGGCCCAAGGCCCGTGGT  605
Db   529  CATATCTHATACAGGCCACTAGCTTACAAAAGGGATTGTAACCCGACCAAAGGCTGTCGT  470

Qy   606  AGCGTTTTGCCTGATGTGGACCATAGCCATTGTTGATCGGCCTGCCTCTCCCTGGGCTG  665
Db   469  TGCGTTTTGTGTGATGTGGACCATCGCCATTGTTCTTCCCGGTCACGACCTCC  410

Qy   666  GAAACTGCGAGAAACTGCAATCTGTTTTGCTCAGACATTGTTCCACACATTGATGAAACCTA  725
Db   409  GAAACTGCAAAGGCTCAACTCTGTGTTCAGACATATTCCCTCTCATCGGATGATGAGAGCTA  350

Qy   726  CCTGAGTTCTGGATCGGGGTCACCGGCTCACCTTCAGACATATTCGTCATCGTGTATGCGGTACAT  785
Db   349  CCTGAGTTCTGGATCGGGGTCACCGGCTCACGTCTTGCTTCCATTGTTCATCGTGGATCGGTGTA  290

Qy   786  GTATAATTCTCTGGGAAGGCCTCACAGCCCACGCCCAGCCACGCCGTCCGACTGGATCCAGGA  845
Db   289  GTACATAACTGTCGGGAGGCCGCACAGCCCACGCCCGTCGGCCATGCTTCAGGGCATGATCCAGGAA  230

Qy   846  GAGCATCATCATCCACACGTCTGAGGATGGGAAGGTAGCAGGTGACCCGGCCGCCAAGGC  905
Db   229  AAGCATAATCATTCAGAGACTACGGGGATGGTAAAGTACAGAGTCACTAGCACTGAGTCAAAC  170

Qy   906  CCGGCATCGGACAGTTAGGTTAGCCAAGACCCTCGTGTCCTGGATGTCTTGGTGGTGTTGATCATCTG  965
Db   169  TCGTATGGACATCAGGTTAGCCAAAAACCTTGGTCCTTATTCTAGTCGTTTAATCATATG  110

Qy   966  CTGGGGGCCCTCGCTTGGCAATCATAGTGGTGTATGATGTCTTGGGGAAGATGAACAAGCTCAT  1025
Db   109  CTCCGGCGCCCTCTTCCGCCATAATGGTGTACGATGTCTTTGGGAAAAATGAACAAGCTCAT  50

Qy  1026  TAAGACCGTGTTTTGCAT  1042
Db    49  CAAGACTGTCTTTCCTT  33
```

AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE   Unpublished (1999)
JOURNAL
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jim Lin, University of Iowa
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
FEATURES   Location/Qualifiers
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                     /dev_stage="embryo 12.5dpc"
                     /clone_lib="NIH_BMAP_F00"
                     /lab_host="DH10B (T1 phage resistant)"
                     /note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
                     Site 2: Not I; The library was constructed according
                     BonaDo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. Denatured RNA was size fractionated on a 1% agarose
                     gel. First strand cDNA synthesis was primed with oligo-dT
                     primer containing a Not I site. Double strand cDNA was
                     size selected according to mRNA size fraction, ligated
                     with EcoR I adaptor, digested with NotI and then cloned
                     directionally into pYX-Asc vector. The library tag
                     sequence located between the Not I site and the polyA tail
                     is TGAGAGACC. This library was created for the University
                     Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
                     Developing Mouse Nervous System', supported by National
                     Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                     program coordinator."
ORIGIN

Query Match   43.3%; Score 571; DB 3; Length 780;
Best Local Similarity   87.4%;
Matches 646; Conservative 0; Mismatches 89; Indels 4; Gaps 2;
                                  Pred. No. 9e-138;

Qy   52 ACTGACCCCTGGGAAGTCCTCTCCAAGAGAGAGAAGAGATGACTGCGGCGGGGACAACCCCCAGCTA 111
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Db   43 ACTTCCTTCAGGGGTAGTCCCTTCCAAGAAAAAGATGACGGCAGGAGACAACTCCCGTTG 102

Qy   112 GTCCCCAGC---AGACCAGGGTGAACATTACAGAATTTTCACACAAGTCTCTCTCGCTCCTTC 168
         || || |||| | |||| | ||| |||||||| ||| | |||||||||||| | ||||
Db   103 GTTCCAGCAGGAGGACACACAACCAACCATTACAGAGTTCTATAACAAGTCTCTCATCGTTC 162

Qy   169 AAGGAGAATGAGGAGACAGAACATCCAGTGTGGGGGAGAAGACTTCAGTGTTTCATG 228
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Db   163 AAGGAGAACGAGGACACAACATCCAGTGTGGGGGAGAAATTTTATGGACACATGGAGTGCTTCATG 222

Qy   229 GTCCTGACCCCAGCCAGCGCTGGCCATTGCAGTCCTGTCCCTCACCCTGGGGCACCTTC 288
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Db   223 ATTCTGAATCCGACCAGCCAGCAGCTGGCCATCGCTGTCCCTGTCCCTCACCCTGGGGCACCTTC 282

Qy   289 ACGGTCCTGGAGGAAACCCCTGTGGCTGCGTGCATCCTCCCACTCCCCGCCTCCGGCTGC 348
         ||||| | |||||||||| |||| |||| | |||||||| ||||||| || || | ||||
Db   283 ACGGTCTCTGGAGGAAACCTCCTGGGTGCTATGTGTCATCCTTCACTCCCGCAGTCCCAGTGC 342

Qy   349 AGGCCTTCCTACCACTTCCATCCGGCAGCCTGGCCGTGGGAGGTGTGCATT 408
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Db   343 AGGCCCTTCCTACCACTTCCATCGGGCAGCCTGGCCGTGGTGGGGAGGTGTCCGATGC 402

Qy   409 TTTGTGTCTCACAGCTTGCATTGACTTCCACGTGTTCCACGTGTTCCACGTGTTT 468
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Db   409 TTTGTGTCTCACAGCTTTGTTGACTTCCACGTGTTCCACGTGTTCCACGTGTTCCCAAATGTGTTT 468

Db   403 TTTGTGTCTCACAGCTTTGTTGACTTCCACGTGTTCCACGTGTTCCACGTGTTCCCAAATGTGTTT 462
Db   469 CTGTTCAAAACTGGGGTGGGGGTCACGGCGGCCTTCCTTCACTCGCCTCCGTGGGCAGCCTGTTCCTC 528
Db   463 CTGTTCAAAACTGGGGTGGGGGTTACCGGCGCCTTCCTTCACAGCATCTGTGGGCAGCCTGTTCCTC 522
Db   529 ACAGCCATCGACAGGTACACATATCCATTCACAGACACGCCCCTGGCCTATAAGAGGAATGTCACC 588
Db   523 ACGGCCATCGACAGGTACACATACCATTCACAGGCCTCTGCCCTATAAGAGGAATCGTCACC 582
Db   589 AGGCCCAAGGCCGTGGTAGGGTTTTGCCTGATGTGACCATPAGCCATTGTGTGATTCGCGTG 648
Db   583 AGGCCCAAGGCCGTAGTGGCCTTTGCCTTGAGTGGGACTATTGCAATAGTAATTGCTAGTG 642
Qy   769 ATCGTGTATGCGTACATGT 787
         ||| ||| |||| | |||||
Db   709 CACATTGATGAAACCTACCTGATGTTCTGGATCGGGGGTCACCAGGCGTACTGCTTCTGTTC 768
Db   703 CTCATTGATGANA--CTACCTGAGTTCTGGATCGGAGTCACCAGTGTGTGCTTGTTGCTGTTC 761
Db   762 ANTGTGTATGCATACATGT 780

RESULT 15
LOCUS   CB520209   789 bp   mRNA   linear   EST 09-JUL-2003
DEFINITION UI-M-GI0-cei-m-16-0-UI.r1 NIH_BMAP_GI0 Mus musculus cDNA clone
            IMAGE:6840089 5', mRNA sequence.
ACCESSION   CB520209
VERSION   CB520209.1 GI:29353564
KEYWORDS   EST.
SOURCE   Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 789)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE   Unpublished (1999)
JOURNAL
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jim Lin, University of Iowa
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/mousefl.html
            This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
FEATURES   Location/Qualifiers
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                     /mol_type="mRNA"
                     /strain="C57BL/6"
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                     /dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
                     /clone_lib="NIH_BMAP_GI0"
                     /lab_host="DH10B (T1 phage resistant)"
                     /note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
                     Site 2: Not I; The library was constructed according
                     BonaDo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. Denatured RNA was size fractionated on a 1% agarose
                     gel. First strand cDNA synthesis was primed with oligo-dT
                     primer containing a Not I site. Double strand cDNA was
                     size selected according to mRNA size fraction, ligated

ORIGIN

with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGGAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

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Query Match
Best Local Similarity    43.2%;     Score 570.8;   DB 4;    Length 789;
Matches  647;  Conservative   87.3%;  Pred. No. 1e-137;
               0;   Mismatches   90;   Indels    4;   Gaps    2;

Qy    52  ACTGACCTTCCTGGGAAGTNCCCTTCCAAGAGAAGGAATGACTGCGGAGGACAACCCCCAGCTA  111
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Db    49  ACTTCCTTCAGGGGTAGTCCCTTCCAAGAAAAAGATGACGGCAGGAGACAACTCCCCGTTG  108

Qy   112  GTCCCAGC---AGACCAGGTGAACATTACAGAATTTTACAACAAGTCTCTCTCTGTCCTTC  168
          ||||||||   | |||||||||||||||||||||||||||||||||||||||||||||||||
Db   109  GTTCCAGGCAGGAGCACAACCAACATTACAGAGTTCTATAACAAGTCTCTCTCATCGTTC  168

Qy   169  AAGGAGAAATGAGGAGGAACATCCAGTGTGGGGGAGAAACTTCATGGACAATAGAGTGTTTCATG  228
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Qy   229  GTCCCTGAACCCCAGCCAGCAGCTGGCCATTGCAGTCTCTCTGTCCCTCAGCCTGGGCACCTTC  288
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Qy   289  ACGGGTCCTGGGAGAACCTTCCTGGTGCTGTGCGTTCATCCTCCACTCCCCGCCAGCCTCCGGCTGC  348
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Qy   349  AGGCCTTCCTACCCACTTCATCGGCAGCCTGGCGGTGGGCGAGAACCTTCCTGGGGAGTGTCATT  408
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Qy   409  TTTGTCTACAGCTTCATTGACTTCCACGTGTTCCACCGCCAAACGTTACCGCAACGTGTTT  468
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Db   409  TTTGTCTACAGCTTTGTTGACTTCCACGTGTTCCACCCGCAAAAGATAGTCCCAAATGTGTTT  468

Qy   469  CTGTTCAAAACTGGGGTGGGGGTCACGGGCCTTCCTTCACTGCCTCCCGTGGGGCCAGCCTGTTCCTC  528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   469  CTGTTCAAAACTGGGTGGGGTTACCGCCTCCTTCACAGCATCTCGTGGGCCAGCCTGTTCCTC  528

Qy   529  ACAGCCCATCGACAGGTACATATCCATTCACAGGCCCTGGCCTATAAGAGGATTGTCACC  588
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   589  AGGCCCAAGGCCCTGGTTAGCGTTTTGCCTGACATGTGGACCATAGCCCATTGTGATCGGCCGTG  648
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Db   589  AGGCCCAAGGCGCTGAGTGGCCCTTTTGCTTGGACTATTGCAAATAGTAAATTGCTGTG  648

Qy   649  CTGCCCTCTTCCTGGGCTGGAACTGGGAGAAACTGGAAATCTGTTTGGCTCAGACAATTTTCCCA  708
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   649  TTGCCTCTCCTGNGCCTGGAACTGCAAGGAGCTGCAAATCTGTTTGCTCAGACACTTCCA  708

Qy   709  C-ACATTGATGAAAACCTACCTGATGTTCTGGAATCGGGGGTCACCAGCGGTACTGCTTCTGTT  767
          |  |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
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Qy   768  CATCGTGTATGCGTACATGTA  788
          ||||||||||||||||||||||
Db   769  CAATGTGTATGCATACATGTA  789
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Job time : 6943 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 16, 2006, 23:32:16 ; Search time 287 Seconds
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Perfect score: 1320
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Scoring table: IDENTITY_NUC
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Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

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Post-processing: Minimum Match 0%
     Maximum Match 100%
     Listing first 45 summaries

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6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1256.2	95.2	2135	3	US-09-016-434-1450	Sequence 1450, Appli
2	1256.2	95.2	2135	3	US-09-023-655-1469	Sequence 1469, Ap
3	1254.6	95.0	1419	3	US-09-826-509-468	Sequence 468, Appl
4	245.2	18.6	1790	3	US-09-016-434-1359	Sequence 1359, Ap
5	245.2	18.6	1790	3	US-09-023-655-1398	Sequence 1398, Ap
6	240.4	18.2	1083	3	US-09-826-509-470	Sequence 470, Appl
7	96.8	7.3	2250	3	US-08-763-938-1	Sequence 1, Appli
8	92.4	7.0	1434	3	US-09-016-434-1310	Sequence 1310, Ap
9	92.4	7.0	1771	3	US-07-969-267B-1	Sequence 1, Appli
10	92.4	7.0	1771	3	US-09-168-510-1	Sequence 1, Appli
11	92.4	7.0	1771	3	US-10-277-078-1	Sequence 1, Appli
12	90.8	6.9	1434	3	US-09-826-509-492	Sequence 492, App
13	90.8	6.9	1673	2	US-07-791-936A-1	Sequence 1, Appli
14	90.8	6.9	1673	3	US-08-383-781B-1	Sequence 1, Appli
15	87	6.9	1535	3	US-09-964-956-14	Sequence 14, Appli
16	85.2	6.5	1621	2	US-08-722-001-13	Sequence 13, Appl
17	85.2	6.5	2002	3	US-09-016-434-1172	Sequence 1172, Ap
18	81.8	6.2	2308	3	US-07-686-591-3	Sequence 3, Appli
19	81.8	6.2	2308	2	US-07-970-715-3	Sequence 3, Appli
20	79.8	6.0	1776	3	US-08-722-001-29	Sequence 29, Appli
21	79.8	6.0	2140	2	US-08-334-698-1	Sequence 1, Appli
22	79.8	6.0	2140	2	US-08-228-932-1	Sequence 1, Appli
23	79.8	6.0	2140	2	US-08-468-939-1	Sequence 24, Appl
24	79.8	6.0	2140	2	US-08-406-855A-1	Sequence 1, Appli
25	79.8	6.0	2140	2	US-08-722-190-1	Sequence 1, Appli
26	79.8	6.0	2140	2	US-08-244-354-1	Sequence 1, Appli
27	79.8	6.0	2140	2	US-09-206-899-1	Sequence 1, Appli
28	79.8	6.0	2140	3	US-09-688-415-1	Sequence 1, Appli
29	79.8	6.0	2140	3	US-09-444-783-1	Sequence 1, Appli
30	79.8	6.0	2140	7	PCT-US99-04203-1	Sequence 1, Appli
31	79.8	6.0	2140	3	US-08-334-698-3	Sequence 3, Appli
32	78	5.9	1738	3	US-08-228-932-3	Sequence 3, Appli
33	78	5.9	1738	2	US-08-468-939-3	Sequence 3, Appli
34	78	5.9	1738	2	US-08-406-855A-3	Sequence 3, Appli
35	78	5.9	1738	2	US-08-722-190-3	Sequence 3, Appli
36	78	5.9	1738	2	US-08-244-354-3	Sequence 3, Appli
37	78	5.9	1738	3	US-09-206-899-3	Sequence 3, Appli
38	78	5.9	1738	3	US-09-444-783-3	Sequence 3, Appli
39	78	5.9	1738	3	US-09-688-415-3	Sequence 3, Appli
40	78	5.9	1738	3	US-09-016-434-1402	Sequence 1402, Ap
41	78	5.9	1738	3	US-09-444-783-3	Sequence 3, Appli
42	78	5.9	1738	3	US-09-688-415-3	Sequence 3, Appli
43	78	5.9	1738	7	PCT-US95-04203-3	Sequence 3, Appli
44	76.4	5.8	921	2	US-08-722-001-17	Sequence 17, Appl
45	76.4	5.8	1567	2	US-08-722-001-24	Sequence 24, App1

ALIGNMENTS

RESULT 1
US-09-016-434-1450
Sequence 1450, Application US/09016434
Patent No. 6500938

GENERAL INFORMATION:

APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1450:
SEQUENCE CHARACTERISTICS:
LENGTH: 2135 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g736236

US-09-016-434-1450

Query Match   95.2%;   Score 1256.2; DB 3; Length 2135;
Best Local Similarity 99.4%;   Pred. No. 8.3e-315;
Matches 1261; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Qy    52 ACTGACCTCCTCTGGGGAAGTCTCCTTCAACAAGAGAAGGAAGATGACTGCGGGGAGGAAGAGGAGGACCAACCCCCAGCTA  111
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   242 ACTTCCTTTAGGGGAAGTCCCTTCCAAGAGAGAAGAGATGACTGCGGGGAGGAAGAGGAGGACCAACCCCCAGCTA       301

Qy   112 GTCCCAGCAGGACCAGGTGAACATTACAGAATTTACAACAAGTCTCTTCTTCGTTCCTTCAAG                      171
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   302 GTCCCAGCAGGACCAGGTGAACATTACAGAATTTACAACAAGTCTCTTCTTCGTTCCTTCAAG                     361

Qy   172 GAGAATGAGGAGGAACATCCAGTGTGGGGAGGAACTTCATGGACATAGAGTGTTTCATGGTC                       231
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   362 GAGAATGAGGAGGAAACATCCAGTGTGGGGAGGAACTTCATGGACATAGAGTGTTTCATGGTC                     421

Qy   232 CTGAACCCCAGCCAGCAGCTGGCCATTGCAGTCGAGTCCTTCCCTGTCCCTCACCCTTCACG                       291
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   422 CTGAACCCCAGCCAGCAGCTGGCCATTGCAGTCGAGTCCTTCCCTGTCCCTCACCCTTCACG                     481

Qy   292 GTCCTGGAGAACCTCCTGGGTGCTGCTCATCCTCCACTCCCGCAGCCTTCCGCTCGGCAGG                        351
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   482 GTCCTGGAGAACCTCCTGGGTGCTGCTCATCCTCCACTCCCGCAGCCTTCCGCTCGGCAGG                      541

Qy   352 CCTTCCTTCACCACTTCATCGGCAGCCTGGCGTGGCAGCCTTCCTCACTCCCGGTCATTTT                        411
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   542 CCTTCCTTCACCACTTCATCGGCAGCCTGGCGTGGCAGCCTTCCTCACTCCCGGTCATTTT                      601

Qy   412 GTCTCAGCTTCATTGACTTCCACGTGTTCACCGCAAAGATTAGCCGCAAACGTGTTTTCTG                        471
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   602 GTCTACAGCTTCATTGACTTCCACGTGTTCACCGCAAAGATTAGCCGCAAACGTGTTTTCTG                      661

Qy   472 TTCAAACTGGGTGGGGTCACGGCGCCTCCTTCACTCACTGCCTCCGTGGGCCAGCCGTTCCTCACA                    531
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   662 TTCAAACTGGGTGGGGTCACGGCGCCTCCTTCACTCACTGCCTCCGTGGGCCAGCCGTTCCTCACA                  721

Qy   532 GCCATCGACAGGTACATATCCATTCACAGGCCCCTGGCCTATAAGAGGATTGTCACCAGG                         591
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   722 GCCATCGACAGGTACATATCCATTCACAGGCCCCTGGCCTATAAGAGGATTGTCACCAGG                        781

Qy   592 CCCAAGGCCGTGGTACCGGTTTTGCCGATGTGGACCATAGCCATTGTGATCGCCGGTGCTG                        651
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   782 CCCAAGGCCGTGGTACCGGTTTTGCCGATGTGGACCATAGCCATTGTGATCGCCGGTGCTG                      841

Qy   652 CCCTCTCCTGGGCTGGAACTGCCGAGAAACTGCAATCTGTTTGCTCAGACATTTTCCCACAC                       711
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   842 CCTCTCCTGGGCTGGAACTGCCGAGAAATCGTTTGCTCAGACATTTTCCCACAC                             901

Qy   712 ATTGATGAAAACCTTACCTGATGTTCTGGATGGGGGGTCACCCAGCGTACTGCCTTCTTCTGTTCATC                  771
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   902 ATTGATGAAAACCTTACCTGATGTTCTGGATGGGGGGTCACCCAGCGTACTGCCTTCTGTTCATC                    961

Qy   772 GTGTATGCGTACATGTATATTCTCTGGAAGGCTCACAGCCTGCCAGCCATGATCAG                             831
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   962 GTGTATGCGTACATGTATATTCTCTGGAAGGCTCACAGCCTGCCAGCCATGATCAG                           1021

Qy   832 CGTGGCACCCAGAAGAGCATCATCATCCACAGTCTGAGGATGGGAGGTACAGGTGACC                          891
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1022 CGTGGCACCCAGAAGAGCATCATCATCCACAGTCTGAGGATGGGAGGTACAGGTGACC                        1081

Qy   892 CGGCCAGACCAAGCCCGCAGTGGACACATTAGGTTAGGCCAAGACCCTGGTCCTGATCCTGGTG                      951
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1082 CGGCCAGACCAAGCCCGCATGGACATTAGGTTAGGCCAAGACCCTGGTCCTGGTG                            1141

Qy   952 GTGTTGATCATCTTGCTCTGGGGCGCCTCTCTCGCTTGCAAATCATCGGTGTATGATGTCTTTTGGGAAG               1011
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1142 GTGTTGATCATCTTGCTCTGGGGCCCCTCTGCTTGCAATCATGGTGTATGATGTCTTTTGGGAAG                   1201

Qy  1012 ATGAACAAGCTCATTAAGACGGTGTTTGCATTCTGCAGTAGCTCTGCCTGCTGAACTCC                         1071
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1202 ATGAACAAGCTCATTAAGACGGTGTTTGCATTCTGCAGTATGTCTCTGCCTGCTGAACTCC                      1261
```

RESULT 2
US-09-023-655-1469
; Sequence 1469, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1469:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2135 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g736236
US-09-023-655-1469

Query Match   95.2%;   Score 1256.2; DB 3; Length 2135;
Best Local Similarity 99.4%;   Pred. No. 8.3e-315;

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Qy  1072 ACCGTGAACCCCATCATCTATATCCTATAGTCTTCTGAGGAGTAAGGAGGACCTTGGCACACAGGCCTTTCCGGAGC        1131
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Db  1262 ACCGTGAACCCCATCCATCATCTATAGTCTCTGAGGAGTAAGGACCTTGGCACACAGGCCTTTCCGGAGC              1321

Qy  1132 ATGTTTCCCTCTTGTTGAAGGGACACTGCCGCAGCCTCTGGATTAACAACTGGAGCCATGGGGGGGGGGGGGACTCGGAC    1191
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1322 ATGTTTCCCTCTTGTTGAAGGGACACTGCCGCAGCCTTCTGGATTAACAGCATGGGGGGGGGGGACTCGGAC            1381

Qy  1192 TGCCTGCACAAACACGCAAAACAATGCACCCAGTGTTCACAGGGGCCATC                                  1251
         ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1382 TGCCTGCACAAACACGCAAAACAATGCACCCAGTGTTCACAGGGGCCATC                                 1441

Qy  1252 AAGAGCACGGTCAAGATTGCCAAGGTAACCAATGTCTGTTCCACAGACGCTGAGAAAAGCTGAG                     1311
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1442 AAGAGCACAGTCAAGATTGCCAAGGTAACCAATGTCTGTTCCACAGACGCTGAGAAAAGCTGAG                    1501

Qy  1312 GCTCTGTGA                                                                          1320
         |||||||||
Db  1502 GCTCTGTGA                                                                          1510
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Query Match   95.2%;   Score 1256.2; DB 3; Length 2135;
Best Local Similarity 99.4%;   Pred. No. 8.3e-315;

Matches 1261; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

RESULT 3
US-09-826-509-468
; Sequence 468, Application US/0982650S
; Patent No. 6806054
; GENERAL INFORMATION:
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 468
; LENGTH: 1419
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-826-509-468

Query Match 95.0%; Score 1254.6; DB 3; Length 1419;
Best Local Similarity 99.3%; Pred. No. 1.7e-314;
Matches 1260; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

[The remainder of the page consists of a Qy/Db nucleotide sequence alignment presented in two columns, with alternating Query (Qy) and Database (Db) rows, base-position numbers at left and right of each row, and vertical bars indicating matched bases.]

RESULT 4
US-09-016-434-1359
Sequence 1359, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490

CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1359:
SEQUENCE CHARACTERISTICS:
LENGTH: 1790 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 9407806
US-09-016-434-1359

Query Match 18.6%; Score 245.2; DB 3; Length 1790;
Best Local Similarity 55.9%; Pred. No. 2.3e-53;
Matches 537; Conservative 0; Mismatches 378; Indels 45; Gaps 2;

Qy   167 TCAAGGAGAATGAGGAGAAACATCCAGTGTGGGGAGAGAACTTCAGTGGACAATAGAGTTCA 226
          ||||||| ||||| |||||| |||| |||||||||| ||||||| |||||||||||
Db   143 TGACAGAGTAGCCAAATGGCTCCAAGGATGGCTTGGAATTCCAACCCTATGAAGGAGATTACA 202

Qy   227 TGGTCCTGGAACCCCAGCCAGCAGCTGGCCATTGCCAGTCCTGTCCCCTCACGGTGGCACCT 286
          |||| |||||||||||||| ||||||||||||||||||||||||||||| |||||
Db   203 TGATCCTGAGTGTGTCCCCAGAAGAGACAGCTGTGTTGCTGTGTTGTCACTCTTCTGGGCTGC 262

Qy   287 TCACGGTCCTGGAGAACCTCCTGGTGCTGTCGGTCATCCTCCACTCCCGGCAGCCTCCGCT 346
          ||||| |||||||||||||||| ||||||||||| |||||||||||||| ||||
Db   263 TAAGTGCCCTGGGAGAACGTGGCTTCTACTGATCCTGTCCCTCCCCACCAACTCCCC 322

Qy   347 GCAGGGCCTTCCTACCACTTCATCGGGCCAGCCTGGCGCGGTGGCCAGAACCTCTGGGGAGTGTCA 406
          |||||||||||||||||||||| |||| |||||||||||||||| ||||||||||
Db   323 GGAAGCCCTCCATACCCGTTCATTGGCAGCTTGGCGTGGGGGCTGACTTCCTGGCCAGTGTGG 382

Qy   407 TTTTTGTCTACAGCTTCATTGACTTCCACGTGTTCCACCGCGAAAGATTAGCCGCAACGTGT 466
          |||| |||||||||||||||||||||| ||||||||||||| ||||||||| ||||||||
Db   383 TCTTTGCATTGCAGCTTTGTTGAAATTTCCATGTTTCCATGGTGGATTCCAAGGCTGTCT 442

Qy   467 TTCTGTTCAAACTGGGGTGGGGTCACGGGCCTCCTTCACTGCCTCCGTGGGGCAGCCTGTTCC 526
          |||||||||||||||||||| ||| |||| |||||||||||||||||||||| ||||||
Db   443 TCCTGCTCGAAGATTGGCAGGCGTGACTAAGCCTTCACAGCCCTCTGTGGGTAGCCTCCTGC 502

Qy   527 TCACAGCCATCGACAGGTACATATCCATTCACAGGGCCCCCTGGCCTATAAGAGGAATTGTCA 586
          ||||||||||| || |||| |||||||||||||| ||| |||||||||||||||||||
Db   503 TGACCGCCATTGACGGATACCTCTGCCCTCCGCTAATCCACCTTCCTACAAAAGCTCTGCTCA 562

Qy   587 CCAGGCCCAAGGCCGTGGTAGCGTTTTCGCCTGATTGAGTGAGGACCATAGCCATTGATCGGCCG 646
          ||||||||| |||| ||||||| ||| ||||||| |||||||||||||| |||| |||||
Db   563 CCCGTGGCGAAGGGCACTGGTGACCCTGGGCCATCAGTGGGTCTTCTCAGCACTAGTCTCCT 622

Db   511 GTCTACAGCTTCATTGACTTCCACGTIGTTCCACCGCGAAAGATTAGCCGCAACGTGTTTCTG 570
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Qy   472 TTCAAACTGGGGTGGGGTCACGGGCCTCCTTCACTGCTTCCACGTGTTCCTCACA 531

Db   571 TTCAAACTGGGTGGGGTCACGGGCCTCCTTCACTGCTTCCGTGGGGCAGCCTGTTCCTCACA 630
          |||||||||| |||||||||||||||||||||||||||||| |||||||||||||
Qy   532 GCCATCGACAGGTACATATCCATTCACAGGGCCCCTGCCTATAAGAGGAATTGTCACCAGG 591

Db   631 GCCATCGACAGGTACATATCCATTCACAGGGCCCCTGCCTATAAGAGGAATTGTCACCAGG 690
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   592 CCCAAGGCCGTGGTAGCGTTTTGCCTGATGTGGACATAGCCATTGTGATCGGCGTGCTG 651

Db   691 CCCAAGGCCGTGGTAGCGTTTTGCCTGATGTGGACCATAGCCATTGTGATCGGCGTGCTG 750
          |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Qy   652 CCTCTCCTGGGCGCTGGGAACTGCGAGAAACTGCAAATCTCTTGTTTGGCTTGCAGGCACAC 711

Db   751 CCTCTCCTGGGCTGGGAACTGCAATCTCTTTGCTCAGACATTTTCCCACAC 810
          ||||||||||| ||||||||||| |||||| |||||| |||||||||||||
Qy   712 ATTGATGAAAACCTACCTGATGTTCTGGATCGGGGTCACCGGTACTGCTTCTGTTCATC 771

Db   811 ATTGATGAAAACCTACCTGATGTTCTGGATCGGGGTCACCGGTACTGCTTCTGTTCATC 870
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Qy   772 GTGTATGCGTACATGTATATTCTTCTGGAAGGGTCCAGCCCAGCCGTCCGCATGATTCAG 831

Db   871 GTGTATGCGTACATGTATATTCTTCTGGAAGGGCTCACAGCCCAGCCGTCCGCATGATTCAG 930
          |||||||||||||||||||||||||||||||| | ||||||||||||||||||||||||||
Qy   832 CGTGGCACCCAGAAGAGCATCATCCACACGCTCTGAGGATGGAAGGTACAGGTGACC 891

Db   931 CGTGGCACCCAGAAGAGCATCATCCACACGCTCTGAGGATGGGAAGGTACAGGTGACC 990
          |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Qy   892 CGGCCAGACCAAGCCCGACATTAGGTTAGCCAAGACACCTGGTCCTGATCCTGGGTG 951

Db   991 CGGCCAGACCAAGCCCCATGACATTAGGTTAAAGAAGACCCGTCCTTGATCCTGGTG 1050
          ||||||||||||||| ||||||||||||| ||||||| ||||||| |||||||
Qy   952 GTGTTGATCATCTGCTGGGGGCCCTCTCGCCTTGCAAATCATGGGTGTATGAGTGTCTTTGGGAAG 1011

Db   1051 GTGTTGATCATCTGCTGGGGGCCCTCTCGCCTTGCAAATCATGGGTGTATGAGTGTCTTTGGGAAG 1110
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1012 ATGAACAAGCTCATTAAGACACGGTGTGTTTGCATTCTCGCAGTATGCTCTCGCTGCTGAACTCC 1071

Db   1111 ATGAACAAGCTCATTAAGACACGGTGTGTTTGCAGTTCTCGCAGTATGCTCTGCCTGCTGAACTCC 1170
          |||||||||||||||||||||||||||||||| ||||||||||||||||||| |||||||||||
Qy   1072 ACCGTGAACCCCATCCATCATCTATCGCTCTGAGGAGTAAGGACACTGGCGACAGCGCTCTTTCCGGAGC 1131

Db   1171 ACCGTGAACCCCATCCATCTATCGCTCTGAGGAGTAAGGACGCTTTCCGGAGC 1230
          |||||||||||||||| ||||||||||||||||||||| |||||| ||||||||
Qy   1132 ATGTTTCCCTCTTGTGAAGGCACTGCGCCAGCCTCTGGATAACAGCATGGGGGACTCGGAC 1191

Db   1231 ATGTTTCCCTCTTGTGAAGGCACTGCGCCAGCCTCTGGATAACAGCATGGGGGACTCGGAC 1290
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1192 TGCCTGCACAAACACGCAAACAAATGCAGCGCAGTTCAGGGCCGGCAGAGAAAGCTGCATC 1251

Db   1291 TGCCTGCACAAACACGCAAACAAATGCAGCGCAGTTCAGGGCCGGCAGAGAAAGCTGCATC 1350
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1252 AAGAGACAGGGTCAAAGATTGCCAAGGTAACCATGTCTGTCCACAGACACACGTCTGCCGAG 1311

Db   1351 AAGAGCACGGTCAAGATTGCCAAGGTAACCATCTCTGTCCACAGACACGTGTGG 1410
          ||||| ||||||||||||||||||||||||||| ||||||||||||||| ||||
Qy   1312 GCTCTGTGA 1320
          |||||||||
Db   1411 GCTCTGTGA 1419

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Qy    647 TGCTGGCTTCTCCTGGGCTGGAGAAACTGGCAATCTGTTTTGCTCAGACATTTTCC 706
          ||||||||| |||||||| ||||||||||||||| ||||||||||||||||||||||
Db    623 ACCTGGCCCTCATGGGATGGGACTTGCTGCTCCCAGGC------CCTGCTCTGAGCTTTTTCC 676

Qy    707 CACACATTGATGAAACCTACCTACTGAGTTCTGGATCGGGGGTCACCAGCGTACTGCTTCTGT 766
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    677 CACTGATCCCAATGACTACCTGCTGAGCTGGCCTTCCTGTTCATCGCCTTCCTCTTTTTCCG 736

Qy    767 TCATCGTGTTATGGGTACATGTATATTCTCTGGAAGGCTCACAGCCACGCGCGGTTCCGCCATGA 826
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    737 GAATCATCTACACCTATGGCATGTTCTCTGGAAGGCCCCATCACCATGTGGCCAGCTT-- 794

Qy    827 TTCAGCGTGGCACCCAGAGAGCAATCATCATCCACACGTCTGAGGATGGGAAGGTACAGG 886
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    795 --------------------------GTCTGGCCACCAGGACAGGCAGG 817

Qy    887 TGACCCGGCCAGACCAAGCCCGCATGGACATTAGGTTACCAAGACCCGTGGTTCCTGATCC 946
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    818 TGCCAGGAATGGCCGGAATGAGGCTGAATGTGAGGTTGGCCAAGACCCTTAGGGTTGT 877

Qy    947 TGGTGGTGGTTGATCATCTGCTGGGGGCCCCTCTGCTTGCAATCATGGTGTATGAGTGTCTTTG 1006
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    878 TGGCTGTTGCTCCTCCATCTGTTGGTTCCCAGTGCTGGCGGCCCTCATGGCCCACATGTGGCCA 937

Qy   1007 GGAAGATGAAACAAGCTCATTAAGACGGTGTTTGCATTCTGCAGTATGCTCTGCTGCTGA 1066
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    938 CTACGCTCAGTGACCAGGTCAAGAAGGCCTTTGCTTTTCTCTCCAAGCTGTGTGCCTCATCA 997

Qy   1067 ACTCCACCGTGAACCCCATCATCATCTTATGTCTTGAGGAGTTAAGGACCTGGACACGGCTTTCC 1126
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    998 ACTCCATGGTCAACCCTGTCATCTATGCTTCTACGGAGTGGAGAGATCCGCCTCTCTCTGCCC 1057
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Query Match    18.6%;  Score 245.2;  DB 3;  Length 1790;
Best Local Similarity  55.9%;  Pred. No. 2.3e-53;
Matches 537;  Conservative 0;  Mismatches 378;  Indels 45;  Gaps 2;

Qy    167 TCAAGGAGAATGAGGAGAACAATCCAGTGTGTGGGGAGGAACTTCATGGACATAGAGTGTTTCA 226
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    443 TGACAGAGATAGCCAAATGGCCTCCAAGGATGGCCTTGGATTCCAACCCTATGAAAGGATTACA 502

Qy    227 TGGGTCCTGAACCCAGCCACAGACTGGCCATTGCAGTGTCCCTGATCCTTCCTCACCGCTGGGCACCT 286
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    203 TGATCCTTGAGTGGTTGTCCCCAGAAGACAGCTGTTGCTGCTGGTGTTGTGCGACTCTTCTGGGCCTGC 262

Qy    287 TCACGGTCCTGGAGAACCCCTGTTGGCGTCATCCTCCACTCCCCGAGCCTCCGGCT 346
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    263 TAAGTGCGCCCTTGGAGGAACGTGGCCTGTTGCTCTATCTGATCCGTGTGGGGGGTGTCA 322

Qy    347 GCAGGCCTTCCTACCCACTTCATCGGCAGCCTGGGGGGTTGGGCAGAACCTCCTTGGGGAGTGTCA 406
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    323 GGAAGCCCTCATACCTGTCATTGGCAGCTGTTGGCGTGGGGGTGACTTCCTGGCAGTGTGG 382

Qy    407 TTTTTGTCTACAGCTTCATTGACTTCCACGGTGTTCCACCGCAAAGTAGCGGCAAGTGT 466
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    383 TCTTTGCATGCAGCTTGTGAATTCCANGTGTTTTCCANGTGTGGGATTCCAAGGCTGTGTCT 442

Qy    467 TTCTGTTCAAAACTGGGTGGGGTCACGGCGTCCTTCCTTCACTGCCTCCGGCCAGCCTGTTCC 526
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    443 TCCTTGCTGAAGATTGGCAGGGTGACGTGACTATGACCTTCACAGCCTTCNTCGTTGGGGGTTAGGCCCTCCGGC 502

Qy    527 TCACAGCCATCGACAGGGTACATATATCCATTCACAGGCCCCTGGCCTTATTAAGGAGGATTGTCA 586
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    503 TGACCGCCATTGACGGAATACCTCTCGCCTCCCTGCCTATCCACCTTTCCTACANAAGCTCTGCTCA 562

Qy    587 CCAGGCCCCAAGGCCCGTGGTAGCGTTTTGCCTGATGCGGACCATAGCCATTGTGATCGCCG 646
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    563 CCCGTGGAAGGGGGCACTCGGTAACCTGGGCATCANGTNGGGTCCTCTCAGCACTAGTCTCCT 622

Qy    647 TGCTGCCTCTCCTGGGGCTGGAACTGCGCGAGAAATCTGTTTTGCTCAGACANTTTTCC 706
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    623 ACCTGGCCCTTCATGGGATGGGACTTGCTGCTCGTCCCAGGC------CCTGCTCTGAGCTTTTTCC 676

Qy    707 CACACATTGATGAAACCTACCTACTGAGTTCTGGATCGGGGGGTCACCAGCGTACTGCTTCTGT 766
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    677 CACTGATCCCAATGACTACCTGCTGAGCTGGCCTTCCTGTTCATCGCCTTCCTCTTTTTCCG 736

Qy    767 TCATCGTGTTATGGGTACATGTATATTCTCTGGAAGGCTCACAGCCACGCGCGGTTCCGCCATGA 826
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    737 GAATCATCTACACCTATGGCATGTTCTCTGGAAGGCCCCATCACCATGTGGCCAGCTT-- 794

Qy    827 TTCAGCGTGGCACCCAGAGAGCAATCATCATCCACACGTCTGAGGATGGGAAGGTACAGG 886
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    795 --------------------------GTCTGGCCACCAGGACAGGCAGG 817

Qy    887 TGACCCGGCCAGACCAAGCCCGCATGGACATTAGGTTAGCCAAGACCCTGGGTTCCTGATCC 946
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    818 TGCCAGGAATGGCCGGAATGAGGCTGAATGTGAGGTTGGCCAAGACCCTTAGGGTTGT 877

Qy    947 TGGTGGTGGTTGATCATCTGCTGGGGCCCCTCTGCTTGCAATCATGGTGTATGAGTGTCTTTG 1006
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    878 TGGCTGTTGCTCCTCCATCTGTTGGTTCCCAGTGCTGGCGGCCCTCATGGCCCACATGTGGCCA 937

Qy   1007 GGAAGATGAAACAAGCTCATTAAGACGGTGTTTGCATTCTGCAGTATGCTCTGCTGCTGA 1066
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    938 CTACGCTCAGTGACCAGGTCAAGAAGGCCTTTGCTTTTCTCTCCAAGCTGTGTGCCTCATCA 997
```

RESULT 6
; US-09-826-509-470
; Sequence 470, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 470
; LENGTH: 1083
; TYPE: DNA
; ORGANISM: Homo sapiens

Query Match   18.2%;   Score 240.4;   DB 3;   Length 1083;
Best Local Similarity 55.6%;   Pred. No. 3.3e-52;
Matches 534;   Conservative 0;   Mismatches 381;   Indels 45;   Gaps 2;

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Qy   1067 ACTCCACCGTGAACCCCATCATTCATTATGCTCTGAGGAGTAAGGACACTGGCGACACGGCTTTCC 1126
          ||||| || | ||||| | ||| |||||| ||||| ||   || |  |  |  |   || ||| ||
Db    998 ACTCCATGGTCAACCCTGTCATCTATGCTCACGGATCGGCTGCTCCTCTGCCC           1057
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Qy   17 ...
Db   ...

(Additional sequence alignment rows from Qy positions 77 through 1126 and corresponding Db positions, representing SEQ ID NO 470.)

RESULT 7
; US-08-763-938-1
; Sequence 1, Application US/08763938
; Patent No. 6140060
; GENERAL INFORMATION:
; APPLICANT: CHUN, Jerold J.M.
; APPLICANT: HECHT, Jonathan H.
; TITLE OF INVENTION: CLONED LYSOPHOSPHATIDIC ACID
; TITLE OF INVENTION: RECEPTORS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray and Oram LLP
; STREET: 655 15th Street, N.W., Suite 330 - G St. Lobby
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/763,938
; FILING DATE: 12-DEC-1996
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: JAHNS, Kristina M.
; REGISTRATION NUMBER: 41,092
; REFERENCE/DOCKET NUMBER: P8074-6018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-5000
; TELEFAX: (202) 638-4810
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2250 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-763-938-1

Query Match   7.3%;   Score 96.8;   DB 3;   Length 2250;
Best Local Similarity 50.5%;   Pred. No. 5.9e-15;
Matches 289;   Conservative 0;   Mismatches 277;   Indels 6;   Gaps 2;

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Qy    551 CACTGATCCCAATGACTACCTGCTGAGCTGGTCCTGTTCATCGCTTCTTCCTCTTTCCG 610
Db    ...
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(Additional sequence alignment rows from Qy positions 551 through 1126 and corresponding Db positions, representing SEQ ID NO 1.)

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Qy    265 CTGTCCCTCACGGTCGGGGCACCTCAGGGTCCTGGAGGAACCTCTTGGGTGCGTGTTGCGGTCATC 324
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    390 CTGGGCATCACTGTTTGCGTGTTCATCATGTTGGCCAATCTCCTTGGGTGCATGGTGCGGCAATC 449

Qy    325 CTCCACTCCCGCAGCCTCCCGGCGCGAGGCCCTGCGGCAGCCTGGGCGGTG 384
          ||||||||||||||||||||   |||||||||||||||||| |||||||||
Db    450 TACGGTCAACCGGCCGCCTTCCATTC---CCTATTTATTACTTGATGGGCCAAACCTGGGCTGCT 506

Qy    385 GCAGACCTCCTGGGGAGTGTGTCATTTTTTGTCTACAGCTTCCACGTGTTCCAC 444
          |||||||||||||||||||||||| | |||||||||||||||||||||||||||
Db    507 GCAGACTTCTTCCGCTGGATTGGCCTACTTCTACCTGATGTTCAATACAGGACCTAAATACC 566

Qy    445 CGCAAAGATAGCCGCAAGTGTTTCTGTTCAAACTGGGTGGGGTCACGGCCCTCCTTCACT 504
          |||||||||||||||||||||||||| |||||| |||||||||||||||||||||||||
Db    567 CGGAGACTGACTGTTAGCACGTGGCTCCCGGCCGCAGGCGCCTCATTGACACCAGCCTGACA 626

Qy    505 GCCTCCGTGGGGCAGCCTGTTCCTCACAGCCATCGACACAGGTAACANATATCCATTCACGAGGCCC 564
          |||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||||||||||
Db    627 GCTTCTCTGGGCCAACCTCGCTATTGCTATCGGAGGAGCACATCACGGTTTTCCGCATG 686

Qy    565 CTGGCCTTATAAGAGGAATTGTCACCAGGCCCCAAGGCCGGTGGTACGTGTTTTGCCTGATGTGTGG 624
          ||||||||||||||||||||||||||||||||||||||||||   ||||||||||||||| ||||||
Db    687 CAGCTCCATCACGGAATGGAGCAAACCGGGGC---GTGGTGGTGGTGATTGGTAGTCATCTGG 743

Qy    625 ACCATAGCCATTGTGATGTCGCCGTGCTCCTCTCCTGGAACTCCGGAGAAACTGCAA 684
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db    744 ACTATGGGCCATTGTGATGGGGCTATACCCAGTGTGGGCTGGAAACTGGCATCTGTGATATC 803

Qy    685 TCTGTTTGCTCAGACACATTTTCCCACACATTGATGAAAACCTACCTGAGTTCTGGGATCGGG 744
          |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db    804 GATCACGTGTTCCAACATGGCACCCCTCTACAGTGGACTCCTACTTAGTGCTTCTTCCGGCCATT 863

Qy    745 GTCACCAGCGTACTGCGTTCTCTGTTCATCGTGATCGGGTACAGTGTATATTCTCTCTGGAAGGCT 804
          |||||||||||| |||||||||||||||||||||||||||||||||||||||| |||||||||||
Db    864 TTCAACCTGGTGACCTTTGTGGGTTCATGGGTTGGTTCTCTACGCTCACATCTTTGGCTATGTT 923

Qy    805 CACAGCCACGCGTCCGCATGANTTCACGGTGG 836
          ||||||||||||||||||||||||||||||||
Db    924 CGCCAGAGGACTATGAGGATGTCTCGGCATAG 955
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Query Match     7.0%;  Score 92.4;  DB 3;  Length 1434;
Best Local Similarity  51.4%;  Pred. No. 6.9e-14;
Matches 213;  Conservative   0;  Mismatches 201;  Indels   0;  Gaps   0;
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Qy    247 CAGCTGGCCATTGCAGTCGTCCTGTTCCCTCACGGTCGGCACCTTCACGGTGTCCTGGAGGAACCTTC 306
          ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    118 CAGGTGGGTCACCGCCTGCCTGCTGCTGAGCCCCTACTCATCATCTGTGACCCTGCTGGGGCAACGGTG 177

Qy    307 CTTGGTGCGTGTTGCGGTCATCCTCCACTCCCGCAGCCTCCCGGCGCGAGGCCTTCCTACCACTTC 366
          ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db    178 CTGGTGTGGCGGCCGCCATCGTCGCGAAGCCCCACCTGCGGCAACATGACCAACGGTCTTC 237

Qy    367 ATCCGGCAGCCTGGGCGGTGGCAGACCTCCTGGGGAGTGTGTCATTTTTTGTCTACAGCTTCATT 426
          ||||| ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    238 ATCGGTGTCTTCTGGGCCGGTGTGACAGCCTTTTCGTGGCGGTCATGGCCGTCCTGGAAGGCA 297

Qy    427 GACTTCCACGTGTTCCACCGGCAAAGATAGCCGCAAGTGTTTCTGTTCAAACTGGGTGGGG 486
          |||||||||||| |||||||||||| |||||||||||||||||||| |||||||||||
Db    298 GTCGCCGAGGTGGCCGGGTTACTGGCCCTTTGGACGGTTCCTGGCAGGCGGTGCCCTTC 357

Qy    487 GTCACGGCCCTCCTTCACTGCCTCCGTGGGGCAGCCTGTTCCTCACAGCCATCGACACAGGTAC 546
          |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db    358 GACATCATGTGCTCCACACTGGCCTCCATCCTGAACCTGTGGGTCATCAGACGTGGACCGGCTAC 417

Qy    547 ATATCCATTCACAGAGGCCCCTGGCCTTATAAGAGGAGATTGGTCACCAGGCCCCAAGGCCGGTGGTA 606
          ||||||||||||| |||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db    418 TGGGCCATCTCAGGAGCCCTTCCGGCTACAGAGCGGCAAGATGAGACTCAGGCGCCTTGGTC 477

Qy    607 GCGTTTTGCCTGATGTGGACCATAGCCATTGTGATCGCGGTGCTGCCTCTCCCTG 660
          ||||| ||||||||||||| ||||||||||||||||||||||||||
Db    478 ATGGTCGGCCTGGCCATGGACCTTGTCATCCTCATCTCCTTCATTCCGGTGCAG 531
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; FILING DATE: 05-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/551,448
; FILING DATE: 10-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 37526-A-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; FEATURE:
; ANTI-SENSE: NO
; HYPOTHETICAL: NO
; MOLECULE TYPE: cDNA
; TOPOLOGY: linear
; STRANDEDNESS: single
; TYPE: nucleic acid
; LENGTH: 1771 base pairs
; SEQUENCE CHARACTERISTICS:
; INFORMATION FOR SEQ ID NO: 1:
; NAME/KEY: CDS
; LOCATION: 140..1573
US-07-969-267B-1

Query Match   7.0%;   Score 92.4;   DB 2;   Length 1771;
Best Local Similarity   51.4%;   Pred. No. 7.4e-14;
Matches 213; Conservative 0; Mismatches 201; Indels 0; Gaps 0;

Qy 247 CAGCTGGCCATTGCAGTCCTGTCCCTCACGCGTGGGGCACCTTCACGGTCCTGAGAACCTC 306
Db 257 CAGGTGGTGTCACCGCCTGCCTGCTCATCCATCTCGACCCTACTCATCATCTGGGCAACGTG 316

Qy 307 CTGGGTGCTGTGGCGTCATCCTTCCACTCCCGCAGCCTCCGCTGCAGGGCCTTCCTACCAC 366
Db 317 CTGGGTGTGGCGAGCCATCGTGCGGAGCCGCCAACCTGGCCTTCCTTACCACTTC 376

Qy 367 ATCGGCAGCCTGGCGGTGGCAGACCTCCTGGGGGAGTGGTCATTTTTGTCTACAGCTTCATT 426
Db 377 ATCGTGTCTCTGGCCGTGTCAGACCTTTTCGTTGGGAGGCGTCATGCCCTGGAAGGCA 436

Qy 427 GACTTCCACGTGTTCACCGCAAAGATAGCCCGCAACGTGTTTCTGTTCAAATCTGGGTGGG 486
Db 437 GTCGCCGAGGTGGCCGGGTACTGCCCTTTGGAGGGTTCTGCCACGTCTGGGTGGCCTTC 496

Qy 487 GTCACGGCGCTCCTTCACTGCCTCCGGTGGGCGACCCGTTCCATCAGCACAGGTAC 546
Db 497 GACATCATGTGTCCACTGCCTCCATCCTGTGGTCATCACGCGTGGACCGCGTAC 556

Qy 547 ATATCCATTCACAGGCCCCCTGGGCCTATAGAGAGGATTGTCACCAGGCCCCAAGGCGTGGGTA 606
Db 557 TGGGCCATCTCCAGGCCCCTTCAGCCCAAGACTGGCCTTGGTC 616

Qy 607 GCGTTTTGCCTGATGTGGACCATAGCCATTGTGATCGCCGTGCTGCTCTCCTG 660
Db 617 ATGGTCGGCCTGGCCATGGACCTTGTCCATCCTCATTCCGGTCCAG 670

RESULT 10
US-09-168-510-1

; Sequence 1, Application US/09168510
; Patent No. 6448767
; GENERAL INFORMATION:
; APPLICANT: Weinshank, Richard L.
; APPLICANT: Hartig, Paul R.
; TITLE OF INVENTION: DNA Encoding A Human Dopamine D1
; TITLE OF INVENTION: Receptor And Uses Thereof
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York

; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/168,510
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,267
; FILING DATE: 05-OCT-1993
; APPLICATION NUMBER: 07/551,448
; FILING DATE: 10-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 37526-A-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1771 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 140..1573
US-09-168-510-1

Query Match   7.0%;   Score 92.4;   DB 3;   Length 1771;
Best Local Similarity   51.4%;   Pred. No. 7.4e-14;
Matches 213; Conservative 0; Mismatches 201; Indels 0; Gaps 0;

Qy 247 CAGCTGGCCATTGCAGTCCTGTCCCTCACGCGTGGGGCACCTTCACGGTCCTGAGAACCTC 306
Db 257 CAGGTGGTGTCACCGCCTGCCTGCTCATCCATCTCGACCCTACTCATCATCTGGGCAACGTG 316

Qy 307 CTGGGTGCTGTGGCGTCATCCTTCCACTCCCGCAGCCTCCGCTGCAGGGCCTTCCTACCAC 366
Db 317 CTGGGTGTGGCGAGCCATCGTGCGGAGCCGCCAACCTGGCCTTCCTTACCACTTC 376

Qy 367 ATCGGCAGCCTGGCGGTGGCAGACCTCCTGGGGGAGTGGTCATTTTTGTCTACAGCTTCATT 426
Db 377 ATCGTGTCTCTGGCCGTGTCAGACCTTTTCGTTGGGAGGCGTCATGCCCTGGAAGGCA 436

Qy 427 GACTTCCACGTGTTCACCGCAAAGATAGCCCGCAACGTGTTTCTGTTCAAATCTGGGTGGG 486
Db 437 GTCGCCGAGGTGGCCGGGTACTGCCCTTTGGAGGGTTCTGCCACGTCTGGGTGGCCTTC 496

Qy 487 GTCACGGCGCTCCTTCACTGCCTCCGGTGGGCGACCCGTTCCATCAGCACAGGTAC 546
Db 497 GACATCATGTGTCCACTGCCTCCATCCTGTGGTCATCACGCGTGGACCGCGTAC 556

Qy 547 ATATCCATTCACAGGCCCCCTGGGCCTATAGAGAGGATTGTCACCAGGCCCCAAGGCGTGGGTA 606
Db 557 TGGGCCATCTCCAGGCCCCTTCAGCCCAAGACTGGCCTTGGTC 616

Qy 607 GCGTTTTGCCTGATGTGGACCATAGCCATTGTGATCGCCGTGCTGCTCTCCTG 660
Db 617 ATGGTCGGCCTGGCCATGGACCTTGTCCATCCTCATTCCGGTCCAG 670

RESULT 11
US-10-277-078-1

; Sequence 1, Application US/10277078
; Patent No. 6939680
; GENERAL INFORMATION:
; APPLICANT: Weinshank, Richard L.
; APPLICANT: Hartig, Paul R.
; TITLE OF INVENTION: DNA Encoding A Human Dopamine D1
;   Receptor And Uses Thereof
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/277,078
; FILING DATE: 21-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/168,510
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 07/969,267
; FILING DATE: 05-OCT-1993
; APPLICATION NUMBER: 07/551,448
; FILING DATE: 10-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 37526-A-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1771 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 140..1573
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-277-078-1

Query Match   7.0%; Score 92.4; DB 3; Length 1771;
Best Local Similarity   51.4%; Pred. No. 7.4e-14;
Matches 213; Conservative   0; Mismatches 201; Indels   0; Gaps   0;

Qy   247 CAGCTGGCCATTGCAGTCTTCCTGCTCCTCACGCTTCCTGGAGAACCTC 306
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Db   377 ATCGTGTCTTCGGCCCGTGTCAGACCTTTTCGTTGGGCCGCTGCTGGTCATGCCCTTCGAAGGCA 436

Qy   427 GACTTCCACGTGTTCACCCGAAAAGATAGCCGCAACGTGTTTCTGTTCAAAACTGGGTGGG 486
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RESULT 12
US-09-826-509-492
; Sequence 492, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
;   Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 492
; LENGTH: 1434
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-509-492

Query Match   6.9%; Score 90.8; DB 3; Length 1434;
Best Local Similarity   51.2%; Pred. No. 1.8e-13;
Matches 212; Conservative   0; Mismatches 202; Indels   0; Gaps   0;

Qy   247 CAGCTGGCCATTGCAGTCTTCCTGCTCCTCACGCTTCCTGGAGAACCTC 306
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Db   118 CAGGTGGTCACCGCCTGCCTGCTGACCCTACTCATCATCATCTGACCCTGCTGGGGCAACGTG 177

Qy   307 CTGGGTGCTGTGGGCTCATCCTCCACTCCCGGCAGCCTTCGCAGGCCTTCCTACCACTTC 366
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Db   178 CTGGGTGCGGCAGGCCATCGTCGCGGACGCCACTCAGGCGCAGGCGTCTTC 237

Qy   367 ATCGGCAGCCTGGCGTGGGCAGACCTCCTGGGGAGTGTCATTTTTGTCTACAGCTTCATT 426
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Qy   607 GCGTTTGCCTGATGTGGACCATAGCCATTGTGATGCGCGGTCCGTTGCTCGCTCCTG 660
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RESULT 13
US-07-791-936A-1

; Sequence 1, Application US/0779l936A
; Patent No. 5427942
; GENERAL INFORMATION:
;   APPLICANT:
;   APPLICANT: Civelli, Olivier
;   APPLICANT: Grandy, David K
;   TITLE OF INVENTION: A No. 5427942el Human Dopamine Receptor Gene and
;   TITLE OF INVENTION: Uses
;   NUMBER OF SEQUENCES: 8
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Allegretti & Witcoff, Ltd.
;   STREET: 10 South Wacker Drive, Suite 3000
;   CITY: Chicago
;   STATE: Illinois
;   COUNTRY: USA
;   ZIP: 60606
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/07/791,936A
;   FILING DATE: 19911113
;   CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;   NAME: MacDonnell, John J
;   REGISTRATION NUMBER: 26,949
;   REFERENCE/DOCKET NUMBER: 91,619
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 312-715-1000
;   TELEFAX: 312-715-1234
;   TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1673 base pairs
;   TYPE: NUCLEIC ACID
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 148..1578
US-07-791-936A-1

Query Match   6.9%; Score 90.8; DB 2; Length 1673;
Best Local Similarity   51.2%; Pred. No. 1.9e-13;
Matches 212; Conservative   0; Mismatches 202; Indels   0; Gaps   0;

Qy   247 CAGCTGGCCATTGCAGTCGTCCCTCACGCTGGGGCACCTTCACGGTCCCTGAGAACCTC 306
               |||| ||||| ||| |||| |||| |||||||| ||| | ||||||||| ||
Db   265 CAGGTGGTCACCCCTGCCTGCTGACCCTACTCATCATCTGGACCCCTGCGGCAACGTG 324

Qy   307 CTGGTGTGCGGTCATCCTCCACTCCCGCAGCCTCCGCGAGGCCTTCCTTACCACTTC 366
               || || ||||||| ||||| ||||| ||| || ||||| || ||| | |||
Db   325 CTGGTGTGCGGCAGCCATCGTGCCGGAGCCGCCAACCTGCGCTCGGTGGGGCCTTC 384

Qy   367 ATCGGCAGCCTGGCGTGGCAGACCTCCTCTGGGGAGTGTCATTTTGTACAGCTTCATT 426
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Qy   487 GTCACGGCCTCCTTCACTGCCTCCGTGGGACCAGCCATCGACACAGGTAC 546
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               ||||| |
Db   565 TGGGCCATCTCCAGGCCCTTCCGGCTACAAGCCGCAAGAGATGACTCAGCGACGGCCGACCTTGGTC 624

Qy   607 GCGTTTTGCCTGATGTGGACCATAGCCATTGTGATCGCCGTGCTGCTCTCCTG 660
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Db   RESULT 14
       US-08-383-781B-1
       ; Sequence 1, Application US/08383781B
       ; Patent No. 5686573
       ; GENERAL INFORMATION:
       ;   APPLICANT:
       ;   APPLICANT: Civelli, Olivier
       ;   APPLICANT: Grandy, David K
       ;   TITLE OF INVENTION: A No. 5686573el Human Dopamine Receptor Gene and
       ;   TITLE OF INVENTION: Uses
       ;   NUMBER OF SEQUENCES: 8
       ;   CORRESPONDENCE ADDRESS:
       ;   ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
       ;   STREET: 300 South Wacker
       ;   CITY: Chicago
       ;   STATE: Illinois
       ;   COUNTRY: USA
       ;   ZIP: 60606
       ;   COMPUTER READABLE FORM:
       ;   MEDIUM TYPE: Floppy disk
       ;   COMPUTER: IBM PC compatible
       ;   OPERATING SYSTEM: PC-DOS/MS-DOS
       ;   SOFTWARE: PatentIn Release #1.0, Version #1.30
       ;   CURRENT APPLICATION DATA:
       ;   APPLICATION NUMBER: US/08/383,781B
       ;   FILING DATE: 06-FEB-1995
       ;   CLASSIFICATION: 530
       ;   ATTORNEY/AGENT INFORMATION:
       ;   NAME: No. 5686573nan, Kevin E
       ;   REGISTRATION NUMBER: 35,303
       ;   REFERENCE/DOCKET NUMBER: 91,619-A
       ;   TELECOMMUNICATION INFORMATION:
       ;   TELEPHONE: 312-913-0001
       ;   TELEFAX: 312-913-0002
       ; INFORMATION FOR SEQ ID NO: 1:
       ;   SEQUENCE CHARACTERISTICS:
       ;   LENGTH: 1673 base pairs
       ;   TYPE: nucleic acid
       ;   STRANDEDNESS: single
       ;   TOPOLOGY: linear
       ;   MOLECULE TYPE: DNA (genomic)
       ;   HYPOTHETICAL: NO
       ;   ANTI-SENSE: NO
       ;   FEATURE:
       ;   NAME/KEY: CDS
       ;   LOCATION: 148..1578
       US-08-383-781B-1

Query Match   6.9%; Score 90.8; DB 2; Length 1673;
Best Local Similarity   51.2%; Pred. No. 1.9e-13;
Matches 212; Conservative   0; Mismatches 202; Indels   0; Gaps   0;

Qy   247 CAGCTGGCCATTGCAGTCGTCCCTCACGCTGGGGCACCTTCACGGTCCCTGAGAACCTC 306
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Db   265 CAGGTGGTCACCCCTGCCTGCTGACCCTACTCATCATCTGGACCCCTGCGGCAACGTG 324

Qy   307 CTGGTGTGCGGTCATCCTCCACTCCCGCAGCCTCCGCGAGGCCTTCCTTACCACTTC 366
               || || ||||||| ||||| ||||| ||| || ||||| || ||| | |||
Db   325 CTGGTGTGCGGCAGCCATCGTGCCGGAGCCGCCAACCTGCGCTCGGTGGGGCCTTC 384

Qy   367 ATCGGCAGCCTGGCGTGGCAGACCTCCTCTGGGGAGTGTCATTTTGTACAGCTTCATT 426
               ||| ||| ||||| ||| |||| ||| ||| |||| |||||||| ||||| ||||
Db   385 ATCGGTGTCTCGGCCGTGTCATGGCGTCGGTCAATGCCCCTGGAAGGCA 444

Qy   427 GACTTCCACGTGTTCACCGGCAAAGATAGCCCGCAACCTTTTCGTGGTCAGCTTCAGT 486
               ||| || || | ||| || ||||| ||| |||| | || | | |||||||||
Db   445 GTCGCCCGAGGTGGCCGGGTTACTGGGCCCTTTGGACGGTCTGGGGTGGCCTTC 504

Qy   487 GTCACGGCCTCCTTCACTGCCTCCGTGGGACCAGCCATCGACACAGGTAC 546
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Db   565 TGGGCCATCCAGCCCTTCCGCGTTACAGAGGCGAAGATGACTCAGCCATGGGCCTTGGTC 624
Qy   607 GCCGTTTTCCTGANGTGTGGACCATAGCCATTGTGATCGGCGGCCGTGTCGCCTCTCCTG 660
Db   625 ATGGTCGGCGCCTGGCCATAGACCTTGTCCATCCTCATCTCCTTCATTCCGGTCCAG 678
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RESULT 15
US-09-964-956-14
Sequence 14, Application US/09964956
Patent No. 6875570

GENERAL INFORMATION:
APPLICANT: Gerlach, Valerie L
APPLICANT: Macdougall, John R
APPLICANT: Smithson, Glenda
APPLICANT: Millet, Isabelle
APPLICANT: Stone, David
APPLICANT: Gunther, Erik
APPLICANT: Ellerman, Karen
APPLICANT: Grosse, William M
APPLICANT: Alsobrook II, John P
APPLICANT: Lepley, Denise M
APPLICANT: Burgess, Catherine E
APPLICANT: Padigaru, Muralidhara
APPLICANT: Kekuda, Ramesh
APPLICANT: Spytek, Kimberly A
APPLICANT: Leach, Martin D
APPLICANT: Shimkets, Richard A

TITLE OF INVENTION: No. 6875570e1 Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-124
CURRENT FILING DATE: 2001-09-26
CURRENT APPLICATION NUMBER: US/09/964,956
PRIOR APPLICATION NUMBER: 60/235,631   PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/235,633   PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/235,808   PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,064   PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,065   PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,066   PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/236,135   PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 60/237,434   PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/238,321   PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/238,399   PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/238,396   PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/276,667   PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/294,823   PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/304,868   PRIOR FILING DATE: 2001-05-31
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 127
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 14
LENGTH: 1535
TYPE: DNA
ORGANISM: Homo sapiens
US-09-964-956-14

Query Match   6.6%;   Score 87;   DB 3;   Length 1535;

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us-10-521-428a-1.rnl   Page 11

Best Local Similarity 50.6%; Pred. No. 1.8e-12;
Matches 210; Conservative 0; Mismatches 205; Indels 0; Gaps 0;

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Qy   366 CATCCGGCAGCCTGGGCGGGGTGGCAGGACCTTCTTCTTGGGGGAGTGTGTCATTTTTTGTCTACAGCTTCAT 425
Db   243 CATCCGTGTCTCTACCTGTGTCAGACCTCTTCGTGTGCGCTCCGTCGTCATGTCCTGAAGGC 302

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Qy   546 CATANTCCATTCACAGAGGCCCCTGGCCTATAAGAGGATTGTTCACCAGGCCCAAGGCCGTGGT 605
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OM nucleic - nucleic search, using sw model

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Post-processing: Minimum Match 0%
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                  Pred. No. is the number of results predicted by chance to have a
                  score greater than or equal to the score of the result being printed,
                  and is derived by analysis of the total score distribution.

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  5      1259.4   95.4    5665  2  AX818167      AX818167 Sequence
  6      1259.4   95.4    5665  5  U73304        U73304 Human CB1 c
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 43      1077.4   81.6    2370  2  HSCB1A        HSCB1A
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                                    U40709        U40709 Mus musculu
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ALIGNMENTS

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RESULT 1
CQ768746

LOCUS       CQ768746               1320 bp    DNA     linear   PAT 04-MAR-2004
DEFINITION  Sequence 1 from Patent WO2004007551.
ACCESSION   CQ768746
VERSION     CQ768746.1  GI:45111938
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Vu,H.K., Groblewski,T. and Greasley,P.
  TITLE     Splice variant cannabinoid receptor (cb1b)
  JOURNAL   Patent: WO 2004007551-A 1 22-JAN-2004;
            Astrazeneca AB (SE)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match      100.0%;  Score 1320;  DB 2;  Length 1320;
Best Local Similarity   100.0%;
Matches 1320;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 ATGAAGTCGATCCTAGATGGCCTTGCAGATACCACACCTTCCGACACCATCACCACTGACCTC 60
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Db          1 ATGAAGTCGATCCTAGATGGCCTTGCAGATACCACACCTTCCGACACCATCACCACTGACCTC 60

Qy         61 CTGGGAAGTCCCTTCCAAGAAGAGATTACTGCCGGGAGACACCCAGTCCCAGCA 120
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Db         61 CTGGGAAGTCCCTTCCAAGAAGAGATTACTGCCGGGAGACACCCAGTCCCAGCA 120

Qy        121 GACCAGGTGAACATTACAGAATTTACAACAAGTCTCTCTCGTCCTTCAAGGAGAAGTAG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GACCAGGTGAACATTACAGAATTTACAACAAGTCTCTCTCGTCCTTCAAGGAGAAGTAG 180

Qy        181 GAGAACATCCAGTGTGGGGAGAACTTCATGGACATAGAGAGTGTTCATGGTCCTGAACCCC 240
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Db   1261 GTCAAGAGGATTTGCCAAAGGTAACCATGTCGTTGTGTCCACAGACACGTTCTGCGAGGCTCTCGTGA 1320

RESULT 2

LOCUS        AY766182              1320 bp    mRNA    linear   PRI 03-JAN-2005
DEFINITION   Homo sapiens cannabinoid receptor 1 splice variant CB1b mRNA,
             complete cds, alternatively spliced.
ACCESSION    AY766182
VERSION      AY766182.1  GI:54609769
KEYWORDS     .
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
REFERENCE    1  (bases 1 to 1320)
  AUTHORS    Ryberg,E., Vu,H.K., Larsson,N., Groblewski,T., Hjorth,S.,
             Elebring,T., Sjogren,S. and Greasley,P.J.
  TITLE      Identification and characterisation of a novel splice variant of
             the human CB1 receptor
  JOURNAL    FEBS Lett. 579 (1), 259-264 (2005)
   PUBMED    15620723
REFERENCE    2  (bases 1 to 1320)
  AUTHORS    Khang Vu,H., Groblewski,T. and Greasley,P.
  TITLE      Direct Submission
  JOURNAL    Submitted (28-SEP-2004) Molecular Sciences, AstraZeneca, 7171
             Frederick Banting, Saint-Laurent, Qc H4S129, Canada
FEATURES             Location/Qualifiers
     source          1..1320
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="6"
                     /map="6q14-q15"
     CDS             1..1320
                     /note="N-terminal variant; alternatively spliced; G
                     protein-coupled receptor"
                     /codon_start=1
                     /product="cannabinoid receptor 1 splice variant CB1b"
                     /protein_id="AAV35030.1"
                     /db_xref="GI:54609770"
                     /translation="MKSILDGLADTTFRTITDLLGSPFQRKWTAGDNPQLVPADQVN
                     ITEFYNKSLSSFKENENINIQQCGENFMDIECFMVLNPSQQLAIAVLSITLGTFTVLENL
                     LVLCVILHSRSLRCRPSYHFIGSLAVADLLGSVIFVYSFIDFHVFHRKDSRNVFLFKL
                     GGVTASFTASVGSLFLTAIDRYISIHRPLAYKRIVTRPKAVVAFCLMWTIAIVIAVLP
                     LLGWNCEKLQSVCSDIFPHIDETYLMFWIGVTSVLLLFIVYAYMYILWKAHSHAVRMI
                     QRGTQKSIIIHTSEDGKVQVTRPDQARMDIRLAKTLVLILVLLICWGPLLAIMVYDV
                     FGKMNKLIKTVFAFCSMLCLLNSTVNPIIYALRSKDLRHAFRSMFPSCEGTAQPLDNS
                     MGDSDCLHKHANNAASVHRAAESCIKSTVKIAKVTMSVSTDTSAEAL"
ORIGIN

Query Match             100.0%;  Score 1320;  DB 5;  Length 1320;
Best Local Similarity   100.0%;
Matches 1320;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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RESULT 3

CS242372

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LOCUS       CS242372                5665 bp    DNA     linear   PAT 09-JAN-2006
DEFINITION  Sequence 24 from Patent WO2005116251.
ACCESSION   CS242372
VERSION     CS242372.1  GI:84657687
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Zimmer,A.
  TITLE     Methods, kits and pharmaceutical compositions for diagnosing,
            delaying onset of, preventing and/or treating osteoporosis
  JOURNAL   Patent: WO 2005116251-A 24 08-DEC-2005;
            YISSUM RESEARCH DEVELOPMENT COMPANY OF THE HEBREW UNIVERSITY OF
            JERUSALEM (IL); INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE
            MEDICALE (INSERM) (FR); Karsak, Meliha (DE); Zimmer, Andreas (DE)
FEATURES             Location/Qualifiers
     source          1..5665
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match          95.4%;  Score 1259.4;  DB 2;  Length 5665;
Best Local Similarity 99.5%;  Pred. No. 0;
Matches 1263;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;
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Qy     52 ACTGACCTCCTGGGAAGTCCCTTCCAAGAAGAAGATGACTGCCGGGGAGACAACCCCAGCTA 111
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Db    272 ACTTCCTTTAGGGGAAGTCCCTTCCAAGAAGAAGATGACTGCCGGGGAGACAACCCCAGCTA 331

Qy    112 GTCCCGACGAGACCAGGTGAAACATTACAGAATTTTACACAGAAGTCTTCTTTCAAG 171
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    332 GTCCCGACGAGACCAGGTGAAACATTACAGAATTTTACACAGAAGTCTTCTTTCAAG 391

Qy    172 GAGAATGAGGAGGAGGAACATCCAGTGTGGGGAGGAGAACTTCATGGGAGAGTTTTCATGGTC 231
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    392 GAGAATGAGGAGGAACATCCAGTGTGGGGAGGAGAACTTCATGGGAGAGTTTTCATGGTC 451

Qy    232 CTGAACCCCAGCCAGCAGCTGGGCCATTGCAGTCCAGTCCTCTGTCCCTCACGGTCAGG 291
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    452 CTGAACCCCAGCCAGCAGCTGGGCCATTGCAGTCCAGTCCTCTGTCCCTCACGGTCACG 511

Qy    292 GTCCTGGAGAAACCTCCTGGTGCGTGGCGTCATCCTCCACTCCCGCAGCCTGCAGG 351
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    512 GTCCTGGAGAAACCTCCTGGTGCGTGGCGTCATCCTCCACTCCCGCAGCCTGCAGG 571

Qy    352 CCTTCCTACCACTTCATCGGCAGCCTGCGGGTGGCAGACCTCCTGGGGAGTGTCATTTTT 411
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Db    572 CCTTCCTACCACTTCATCGGCAGCCTGCGGGTGGCAGACCTCCTGGGGAGTGTCATTTTT 631

Qy    412 GTCTACAGCTTCATTGACTTGACTTCCACGTGTTCCACGGCAAAGATAGCCGGCAAACGTGTTTCTG 471
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    632 GTCTACAGCTTCATTGACTTCCACGTGTTCCACGGCAAAGATAGCCGGCAAACGTGTTTCTG 691

Qy    472 TTCAAAACTGGGGTGGGGTCACGGCGTCCTCGCTCCTTCACTGCCTCCGGTGGGCAGCCTGTTCCTCACA 531
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    692 TTCAAAACTGGGGTGGGGTCACGGCGTCCTCGCTCCTTCACTGCCTCCGGTGGGCAGCCTGTTCCTCACA 751

Qy    532 GCCATCGACAGGTACATATCCATTCACAGGCCCCTGGCCTATAAGAGCAATTGTCACCAGG 591
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    752 GCCATCGACAGGTACATATCCATTCACAGGCCCCTGGCCTATAAGAGCAATTGTCACCAGG 811

Qy    592 CCCAAGGCCGTGGTAGCGTTTGCCTGATGTGGAACCATTGTGATCTGGCTG 651
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    812 CCCAAGGCCGTGGTAGCCGTTTTGCCTGATGTGGAACCATTGTGATCGGGCTG 871

Qy    652 CCTCTCCTGGGCTGGGGACTGCAGAAACTGCAAATCTGTTTGCTCAGACATTTTCCCACAC 711
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    872 CCTCTCCTGGGCTGGGGACTGCGAGAAACTGCAATCTGTTTTGCTCAGACATTTTCCCACAC 931
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Db    241 AGGCAGCAGCAGGCTGGGCCATTGCAGTCCAGTCCTCTGTCCCTCACGCGCTGGGCACTTCACGGTCCTGGAG 300
Qy    301 AACCTCCTGGTGTGTTCGGTCATCCTCCACTCCCGCAGCCTGCAGG 360

Db    361 CACTTCATCGGCAGCCTGGCGGTGGCAGACCTCCTGGGGAGTGTCATTTTTGTCTACAGC 420
Db    481 GGTGGGGGTCACGGCGCCTCCTTCACTGCCTCCGGTGGGCAGCCTGTTCCTCACAGCCATCGAC 540
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RESULT 4
AX658255
LOCUS       AX658255               5665 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 171 from Patent WO03000928.
ACCESSION   AX658255
VERSION     AX658255.1  GI:29160783
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Poulsen,H.S., Pedersen,N., Mortensen,S., Sorensen,S.B.,
            Petersen,M.W. and Elsner,H.I.
  TITLE     Methods for identification of cancer cell surface molecules and
            cancer specific promoters, and therapeutic uses thereof
  JOURNAL   Patent: WO 03000928-A 171 03-JAN-2003;
            Odin Medical A/S (DK)
FEATURES             Location/Qualifiers
     source          1..5665
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match             95.4%;  Score 1259.4;  DB 2;  Length 5665;
                        Best Local Similarity   99.5%;  Pred. No. 0;
  Matches 1263;  Conservative 0;  Mismatches 0;  Indels 6;  Gaps 0;

Qy        712 ATTGATGAAACCTACCTGATGTTCTGGATCGGGGTCACCAGCGTACTGCTTCGTTCATC 771
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Db         52 ACTGACCTCCTGGGACTCCCTTCCAAGGAGAAGCGTACTGCTTCGTTCATC 111

Qy        932 ATTGATGAAACCTACCTGATGTTCTGGATCGGGGTC 991
              |||||||||||||||||||||||||||||||||||
Db        272 ACTTCCTTTAGGGGACGTCCCTTCCAAGAAGAGAAGATGACTGCGGGAGAACCCCAGCTA 331

Qy        772 GTGTATCGGTACATGTATATTCTCTGGAAGGCTCACCAGCCACCAGCGTACTCAGATTCAG 831
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GTCCCAGCAGACCAGGTGAACATTACAGAATTTTACAACAAGTCTCTCGGTCCTTCAAG 391

Qy        992 GTGTATCGGTACATGTATATTCTCTGGAAGGCTCACCAGCCACCAGCGTACTCAGATTCAG 1051
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Db        112 GTCCCAGCAGACCAGGTGAACATTACAGAATTTTACAACAAGTCTCTCGGTCCTTCAAG 171

Qy        832 CGTGGGCACCCAGAGAGCACATCATCATCCACACGTCTGAGGATGGGAAGGTACAGGTGACC 891
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GTCCCAGCAGACCAGGTGAACATTACAGAATTTTACAACAAGTCTCTCGGTCCTTCAAG 391

Qy       1052 CGTGGGCACCCAGAGAGCACATCATCATCCACACGTCTGAGGATGGGAAGGTACAGGTGACC 1111
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Db        172 GAGAATGAGGAGGAACATCCAGTGTGGGGAGAACTTCATGGACATAGAGTGTTTCATGGTC 231

Qy        892 CGGCCAGACCAAGCCCGCCATGGACATCATCCAGTGTTGGAAGGTACCAGGTGACC 951
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 GAGAATGAGGAGGAACATCCAGTGTGGGGAGAACTTCATGGACATAGAGTGTTTCATGGTC 451

Qy       1112 CGGCCAGACCAAGCCCGCCATGGACATCATCCAGTGTTGGAAGGTACCAGGTGACC 1171
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Db        232 CTGGAAACCCCAGCCAGCGAGCTGTGCAGCTGGGCCATTGCAGTGTTGGGAGATGC 291

Qy        952 GTGTTGATCAGTCTGCTGCTGGGGGTG 1011
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Db        452 CTGGAAACCCCAGCCAGCGAGCTGTGCAGCTGGGCCATTGCAGTGTTGGGAGATGC 511

Qy       1172 GTGTTGATCAGTCTGCTGCTGGGGGTG 1231
              |||||||||||||||||||||||||||
Db        292 GTCCTGGAGAACCTTCATCGGTGCTGTGTCCAGAGTCATCCTCCACTCCCGGCAGG 351

Qy       1012 ATGAACAAGCTCATTAAGACGGTTG 1071
              |||||||||||||||||||||||||
Db        512 GTCCTGGAGAACCTTCATCGGTGCTGTGTCCAGAGTCATCCTCCACTCCCGGCAGG 571

Qy       1232 ATGAACAAGCTCATTAAGACGGTTG 1291
              |||||||||||||||||||||||||
Db        352 CCTTCCTACCACTTCATCGGCAGCCTGGCGGTGGCCAGAACCCTCCTGGGGAGTGTGCATTTT 411

Qy       1072 ACCGTGAACCCCATCATCATCTAT 1131
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Db        572 CCTTCCTACCACTTCATCGGCAGCCTGGCGGTGGCCAGAACCCTCCTGGGGAGTGTGCATTTT 631

Qy       1292 ACCGTGAACCCCATCATCATCTAT 1351
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Db        412 GTCTACAGCTTCATTGACTTCACAGTGTTCACAGCAAAGATAGCCCCCAAACGTGTTTCTG 471

Qy       1132 ATGTTTCCCTCTTGTGTGAAGGACT 1191
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Qy       1352 ATGTTTCCCTCTTGTGTGAAGGACT 1411
              |||||||||||||||||||||||||
Db        472 TTCAAACTGGGTGGGGGTCACGGGCCTCCTTCACTGCCTCCGGTGGGCGTGGGTGTTCACA 531

Qy       1192 TGCCTGCACAAACACCCAAACAACA 1251
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Db        692 TTCAAACTGGGTGGGGGTCACGGGCCTCCTTCACTGCCTCCGGTGGGCGTGGGTGTTCACA 751

Qy       1412 TGCCTGCACAAACACCCAAACAACA 1471
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Db        532 GCCATCAGCTACAGGTACATATCCATTCACAGGGCCCCTGGCCTATAAGGAGGATTGGTCACCAGG 591

Qy       1252 AAGAGACACGGTCAAGATTGCCAAG 1311
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Db        752 GCCATCAGCTACAGGTACATATCCATTCACAGGGCCCCTGGCCTATAAGGAGGATTGGTCACCAGG 811

Qy       1472 AAGAGACACGGTCAAGATTGCCAAG 1531
              |||||||||||||||||||||||||
Db        592 CCCAAGGCCGTGGGTAGCCGTTTTGCCCTGATGTGACCATAGCCATTGTGATCTCCCGTGCTG 651

Qy       1312 GCTCTCGTGA 1320
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Db        812 CCCAAGGCCGTGGGTAGCCGTTTTGCCCTGATGTGACCATAGCCATTGTGATCTCCCGTGCTG 871

Qy       1532 GCTCTCGTGA 1540
              ||||||||||
Db        652 CCTCTCCTGGGCGTGGAACTGCGAGAAACTGCAATCTGTTGTTGCTCAGACATTTTCCACAC 711

Db        872 CCTCTCCTGGGCGTGGAACTGCGAGAAACTGCAATCTGTTGTTGCTCAGACATTTTCCACAC 931
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RESULT 5

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LOCUS       AX818167    5665 bp    DNA    linear    PAT 10-DEC-2003
DEFINITION  Sequence 38 from Patent WO03068268.
ACCESSION   AX818167
VERSION     AX818167.1  GI:39723240
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ek,S., Borrebaeck,C.A. and Ehinger,M.
  TITLE     Treatment&comma; diagnosis and imaging of disease
  JOURNAL   Patent: WO 03068268-A 38 21-AUG-2003;
            BIOINVENT INTERNATIONAL AB (SE)
FEATURES            Location/Qualifiers
     source         1..5665
                    /organism="Homo sapiens"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:9606"
ORIGIN

Query Match            95.4%;  Score 1259.4;  DB 2;  Length 5665;
Best Local Similarity  99.5%;  Pred. No. 0;  Mismatches 0;
Matches 1263;  Conservative 0;  Mismatches 6;  Indels 0;  Gaps 0;
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Qy     52 ACTGACCTCCTCGGAGT...                              111
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Db    632 GTCTACAGCTTCATTGACTTCCACGT...                    691
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RESULT 6

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LOCUS       HSU73304    5665 bp    DNA    linear    PRI 05-NOV-1996
DEFINITION  Human CB1 cannabinoid receptor (CNR1) gene, complete cds.
ACCESSION   U73304
VERSION     U73304.1  GI:1657840
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 5665)
AUTHORS     Hoehe,M.R., Caenazzo,L., Martinez,M.M., Hsieh,W.T., Modi,W.S.,
            Gershon,E.S. and Bonner,T.I.
TITLE       Genetic and physical mapping of the human cannabinoid receptor gene
            to chromosome 6q14-q15
JOURNAL     New Biol. 3 (9), 880-885 (1991)
PUBMED      1931832
REFERENCE   2  (bases 1 to 5665)
AUTHORS     Bonner,T.I.
TITLE       The coding exon of the human CB1 cannabinoid receptor
JOURNAL     Unpublished
REFERENCE   3  (bases 1 to 5665)
AUTHORS     Bonner,T.I.
TITLE       Direct Submission
JOURNAL     Submitted (03-OCT-1996) Lab of Cell Biology, NIMH, Bldg. 36, Rm
            3A-17, MSC 4090, Bethesda, MD 20892-4090, USA
FEATURES             Location/Qualifiers
source          1..5665
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"
                /chromosome="6"
                /map="6q14-15"
intron          <1..58
                /note="5 exons located 19-23 kb upstream"
gene            59..5530
                /gene="CNR1"
mRNA            <59..5530
                /gene="CNR1"
CDS             122..1540
                /gene="CNR1"
                /note="G protein-coupled receptor"
                /codon_start=1
                /product="CB1 cannabinoid receptor"
                /protein_id="AAB18200.1"
                /db_xref="GI:1657841"
                /translation="MKSILDGLADTTFRTITTDLLYVGSNDIQYEDIKGDMASKLGYF
                PQKFPLTSFRGSPFQEKMTAGDNPQLVPADQVNITEFYNKSLSSFKENENIQCGENF
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                VADLLGSVIFVYSFIDFHVFHRKDSRNVFLFKLGGVTASFTASVGSLFLTAIDRYISI
                HRPLAYKRIVTRPKAVVAFCLMWTIAIVIAIVPLLGWNCEKLQSVCSDIFPHIDETYL
                MFWIGVTSVLLLFIVYAYMYILWKAHSHAVRMIQRGTQKSIIIHTSEDGKVQVTRPDQ
                ARMDIRLAKTIVLILVVLIICWGPLLAIMVYDVFGKMNKLIKTVFAFCSMLCLLNSTV
                NPIIYALRSKDLRHAFRSMFPSCEGTAQPLDNSMGDSDCLHKHANNAASVHRAAESCI
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polyA_signal    5499..5504
                /gene="CNR1"
polyA_site      5530
                /gene="CNR1"
                /note="location established by comparison with ESTs with
                GenBank Accession Numbers R20626, R42346, H06205, H10202"
ORIGIN

Query Match     95.4%;  Score 1259.4;  DB 5;  Length 5665;
Best Local Similarity   99.5%;  Pred. No. 0;
Matches 1263;  Conservative   0;  Mismatches   6;  Indels   0;  Gaps   0;
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Qy      52 ACTGACCTCCTGGGAGTCCCTTCCCAGAGAGAAGATGACTGCGGGAGGACAACCCCAGCTA 111
           ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db     452 CTGAACCCCAGCCAGCAGCTGGCCATTGCAGTCCTGTCCCTCAGCGTGGGCACCTTCACG 511

Qy     272 ACTTCCTTTAGGGGAGGAAGTCCCTTCCAAGAGAAGATGACTGCGGGAGGACAACCCCAGCTA 331
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     292 GTCCTGGAGGAACCTTCCTTGGGTGGCTGGTGGGCAGGACCTCATCGTCCTCATCTCCAGG 351

Qy     112 GTCCCAGCAGCCAGGTGAACATTACAACAAGTCTCTCCTTCAAGAGAAGATGACTGCGGG 171
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Db     512 GTCCTGAGAAACCTCCTCGGGTGGCTGGTGGGCAGGACCTCATCCTCCGACTCCGACGCAGG 571

Qy     332 GTCCCAGCAGCCAGGTGAACATTACAACAAGTCTCTCCTTCAAG 391
           ||||||||||||||||||||||||||||||||||||||||||||
Db     352 CCTTCCTTACCCACTTCATCGGCAGCCCTGCGGTGGCAGACCTTC 411

Qy     172 GAGAATGAGGAGGAAGAACATCCAGTGTGTGGGGGAGAGTGTTTTCATCGTC 231
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Db     572 CCTTCCTTACCCACTTCATCGGCAGCCCTGCGGTGGCAGACCTTCTGGGGGAGTGTCATTTT 631

Qy     392 GAGAATGAGGAGGAACATCCAGTGTGGGGAGAACTTCATGGACATAGAGAGTGTTTCATGGTC 451
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Db     412 TTCAAACTGGGTGGGGTCACGGCCTCCTTCACTGCTTCACTCGGTCCTCACACGTTTCTG 471

Qy     232 CTGAACCCCAGCCAGCAGCTGGCCATTGCAGTCCTGTCCCTCAGCGTGGGCACCTTCACG 291
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1532 GCTCTGTGA 1540
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RESULT 7
AY225225
LOCUS           AY225225                1419 bp    DNA     linear   PRI 27-MAR-2003
DEFINITION      Homo sapiens cannabinoid receptor 1 long isoform gene, complete
                cds.
ACCESSION       AY225225
VERSION         AY225225.1  GI:29293104
KEYWORDS        .
SOURCE          Homo sapiens (human)
  ORGANISM      Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Hominidae; Homo.
REFERENCE       1  (bases 1 to 1419)
  AUTHORS       Kopatz,S.A.; Aronstam,R.S. and Sharma,S.V.
  TITLE         Isolation of complete coding sequence for cannabinoid receptor 1
                long isoform (CNR1L)
  JOURNAL       Unpublished
REFERENCE       2  (bases 1 to 1419)
  AUTHORS       Kopatz,S.A.; Aronstam,R.S. and Sharma,S.V.
  TITLE         Direct Submission
  JOURNAL       Submitted (21-JAN-2003) Guthrie cDNA Resource Center, Guthrie
                Research Institute, 1 Guthrie Square, Sayre, PA 18840, USA
FEATURES             Location/Qualifiers
     source          1..1419
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     mRNA            <1..>1419
                     /product="cannabinoid receptor 1 long isoform"
     CDS             1..1419
                     /note="G-protein coupled receptor; CNR1L"
                     /codon_start=1
                     /product="cannabinoid receptor 1 long isoform"
                     /protein_id="AAO67710.1"
                     /db_xref="GI:29293105"
                     /translation="MKSILDGLADTIFRTITTDLLYVGSNDIQYEDIKGDMASKLGYF
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                     VADLLGSVIFVYSFIDFHVFHRKDSRNVFLFKLGGVTASFTASVGSLFLTAIDRYISI
                     HRPLAYKRIVTRPKAVVAFCLMWTIAIVIAVLPLLGWNCEKLQSVCSDIFPHIDETYL
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ORIGIN

Query Match          95.3%;  Score 1257.8;  DB 5;  Length 1419;
Best Local Similarity   99.4%;  Pred. No. 0;  Mismatches 7;  Indels 0;  Gaps 0;
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RESULT 8
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LOCUS   BC100968
DEFINITION   Homo sapiens cannabinoid receptor 1   1419 bp   mRNA   linear   PRI 02-AUG-2005
                (brain), transcript variant 1,

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ACCESSION BC100968
VERSION   BC100968.1  GI:71682702
KEYWORDS  MGC.
SOURCE    Homo sapiens (human)
  ORGANISM Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
           Hominidae; Homo.
REFERENCE 1  (bases 1 to 1419)
  AUTHORS  Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
           Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
           Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
           Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
           Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
           Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
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           Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
           McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
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           Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
           Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
           Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
           Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM  Mammalian Gene Collection Program Team
  TITLE    Generation and initial analysis of more than 15,000 full-length
           human and mouse cDNA sequences
  JOURNAL  Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  PUBMED   12477932
REFERENCE 2  (bases 1 to 1419)
  CONSRTM  NIH MGC Project
  TITLE    Direct Submission
  JOURNAL  Submitted (01-AUG-2005) National Institutes of Health, Mammalian
           Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT    Contact: MGC help desk
           Email: cgapbs-r@mail.nih.gov
           Tissue Procurement: Baylor Human Genome Sequencing Center
           cDNA Library Preparation: Baylor Human Genome Sequencing Center
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Sequencing Group at the Stanford Human Genome
           Center, Stanford University School of Medicine, Stanford, CA 94305
           Web site: http://www-shgc.stanford.edu
           Contact: (Dickson, Mark) mcd@paxil.stanford.edu
           Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
           R. M.
           Clone distribution: MGC clone distribution information can be found
           through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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ORIGIN
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Query Match   95.3%;   Score 1257.8;   DB 5;   Length 1419;
Best Local Similarity   99.4%;   Pred. No. 0;
Matches 1262;   Conservative 0;   Mismatches 7;   Indels 0;   Gaps 0;

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RESULT 9
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DEFINITION   Homo sapiens cannabinoid receptor 1 (brain), transcript variant 1,
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ACCESSION   BC100969
VERSION   BC100969.1 GI:71680856
KEYWORDS   MGC.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
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              Hominidae; Homo.
REFERENCE   1 (bases 1 to 1419)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
              Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
              Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
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  CONSRTM   Mammalian Gene Collection Program Team
  TITLE   Generation and initial analysis of more than 15,000 full-length
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  PUBMED   12477932
REFERENCE   2 (bases 1 to 1419)
  AUTHORS   .
  CONSRTM   NIH MGC Project
  TITLE   Direct Submission
  JOURNAL   Submitted (01-AUG-2005) National Institutes of Health, Mammalian
              Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT   Contact: MGC help desk
              Email: cgapbs-r@mail.nih.gov
              Tissue Procurement: Baylor Human Genome Sequencing Center
              cDNA Library Preparation: Baylor Human Genome Sequencing Center
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Sequencing Group at the Stanford Human Genome
              Center, Stanford University School of Medicine, Stanford, CA 94305
              Web site: http://www-shgc.stanford.edu
              Contact: (Dickson, Mark) mcd@paxil.stanford.edu
              Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
              R. M.
              Clone distribution: MGC clone distribution information can be found
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ORIGIN
Query Match   95.3%; Score 1257.8; DB 5; Length 1419;
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Qy          412 GTCTACAGCTTCATTGACTTCATTCCACAGGATAGCCGCAAAGACGTGTTTTCTG 471
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RESULT 10

BC074811

LOCUS   BC074811   1492 bp   mRNA   linear   PRI 16-AUG-2004
DEFINITION   Homo sapiens cannabinoid receptor 1 (brain), transcript variant 1,
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ACCESSION   BC074811
VERSION   BC074811.2 GI:50959691
KEYWORDS   MGC.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Hominidae; Homo.
REFERENCE   1 (bases 1 to 1492)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
                Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
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                Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
                Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
                Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
                Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
                Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
                Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
                Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE   Generation and initial analysis of more than 15,000 full-length
                human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2 (bases 1 to 1492)
  AUTHORS   Strausberg,R.L.
  TITLE   Direct Submission
  JOURNAL   Submitted (25-JUN-2004) National Institutes of Health, Mammalian
                Gene Collection (MGC), Cancer Genomics Office, National Cancer
                Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                USA
REMARK   NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT   On Aug 4, 2004 this sequence version replaced gi:49901676.
                Contact: MGC help desk
                Email: cgapbs-r@mail.nih.gov
                Tissue Procurement: Genome Sequence Centre, British Columbia Cancer
                Center
                cDNA Library Preparation: British Columbia Cancer Research Center
                cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                DNA Sequencing by: Genome Sequence Centre,
                BC Cancer Agency, Vancouver, BC, Canada
                info@bcgsc.bc.ca
                Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
                Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
                Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
                Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
                Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prabhu,
                Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska,
                Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie
                Schein, Asim Siddiqui, Rob Holt, Marco Marra.
                Clone distribution: MGC clone distribution information can be found
                through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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           NPIIYALRSKDLRHAFRSMFPSCEGTAQPLDNSMGDSDCLHHANNAASVHRAAESCI
           KSTVKIAKVTMSVSTDTSAEAL"
ORIGIN
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Best Match

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Query Match      95.3%;  Score 1257.8;  DB 5;  Length 1492;
Best Local Similarity   99.4%;  Pred. No. 0;  Mismatches 7;  Indels 0;  Gaps 0;
Matches 1262;  Conservative 0;  Mismatches 7;  Indels 0;  Gaps 0;
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Db  189 ACTTCCTTTAGGGAGGAGTCCCTTCCAAGAAGAAGATGACTGCGGGAGACAAACCCCAGCTA 248

Qy  112 GTCCCAGCAGACCAGGTGAACATTACAGAGAATTTTACAACAAGTCTCTTCGTCCTTCAAG 171
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TITLE            Generation and initial analysis of more than 15,000 full-length
                 human and mouse cDNA sequences
JOURNAL          Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED           12477932
REFERENCE        2  (bases 1 to 1492)
AUTHORS          Direct MGC Project.
TITLE            Direct Submission
JOURNAL          Submitted (25-JUN-2004) National Institutes of Health, Mammalian
                 Gene Collection (MGC), Cancer Genomics Office, National Cancer
                 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                 USA
REMARK           NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT          On Aug 4, 2004 this sequence version replaced gi:4990249.
                 Contact: MGC help desk
                 Email: cgapbs-r@mail.nih.gov
                 Tissue Procurement: Genome Sequence Centre, British Columbia Cancer
                 Center
                 cDNA Library Preparation: British Columbia Cancer Research Center
                 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                 DNA Sequencing by: Genome Sequence Centre,
                 BC Cancer Agency, Vancouver, BC, Canada
                 info@bcgsc.bc.ca
                 Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
                 Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
                 Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
                 Kim Macdonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
                 Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prabhu,
                 Paraneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska,
                 Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie
                 Schein, Asim Siddiqui, Rob Holt, Marco Marra.

                 Clone distribution: MGC clone distribution information can be found
                 through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                 Series: IRBU Plate: 4 Row: G Column: 5.
FEATURES             Location/Qualifiers
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                     /clone="MGC:104081 IMAGE:30915532"
                     /tissue_type="Lung, PCR rescued clones"
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                     /db_xref="MIM:114610"
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                     /protein_id="AAH74812.1"
                     /db_xref="GI:49902500"
                     /db_xref="GeneID:1268"
                     /db_xref="MIM:114610"
                     /translation="MKSILDGLADTTFRTITTDLLYVGSNDIQYEDIKGDMASKLGYF
                     PQKFPLTSFRGSPSFQEKMTAQDNPLVPADQVNITEFYNKSLSSFKENEENIQCGENF
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                     VADLLGSVIFVYSFIDFHVFRRKDSRNVFLFKLGGVTASFTASVGSLFLTAIDRYISI
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            Query Match      95.3%;   Score 1257.8;  DB 5;  Length 1492;
            Best Local Similarity   99.4%;   Pred. No. 0;
            Matches 1262;  Conservative   0;  Mismatches   7;  Indels   0;  Gaps   0;

Qy    52  ACTGACCTTCCTGGGAAGTCCCTTCCAAGAAGAAGAGATGAGACTGCCGGGGACAGCTA  111
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Db   189  ACTTCCTTTAGGGGAAGTCCCTTCCAAGAAGAAGAGATGAGACTGCCGGGGACAGCTA  248

Qy   112  GTCCCAGCAGCCAGGGTGAACATTACAGAGAATTTTACAACAAGTCTCTCTGCGTCCTTCAAG  171
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Db   249  GTCCCAGCAGCCAGGGTGAACATTACAGAGAATTTTACAACAAGTCTCTCTGCGTCCTTCAAG  308

Qy   172  GAGAATGAGGAGAACATCCAGTGTGGGGAGAACTTCATGGACATAGAGTGTTTCATGGTC  231
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Db   309  GAGAATGAGGAGAACATCCAGTGTGGGGAGAACTTCATGGACATAGAGTGTTTCATGGTC  368

Qy   232  CTGAACCCCAGCCAGCAGCTGGCCATTGCAGTGCTGTCCCTGACGCTGGGCACCTTCACG  291
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Db   369  CTGAACCCCAGCCAGCAGCTGGCCATTGCAGTGCTGTCCCTGACGCTGGGCACCTTCACG  428

Qy   292  GTCCTGGAGAACCTTCTGGTGCTGTGCGTCATCCTGCACTCTCGCAGCCTCCGCTGCAGG  351
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Db   429  GTCCTGGAGAACCTTCTGGTGCTGTGCGTCATCCTGCACTCTCGCAGCCTCCGCTGCAGG  488

Qy   352  CCTTCCTACCACTTCATCGGCAGCCTGGCCGTGGCAGACCTCCTGGGGAGTGTCATTTTT  411
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Db   489  CCTTCCTACCACTTCATCGGCAGCCTGGCCGTGGCAGACCTCCTGGGGAGTGTCATTTTT  548

Qy   412  GTCTACAGCTTCATTGACTTCCACGTGTTCCACCGGAAAGATAGCCGCAACGTGTTTCTG  471
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Db   549  GTCTACAGCTTCATTGACTTCCACGTGTTCCACCGGAAAGATAGCCGCAACGTGTTTCTG  608

Qy   472  TTCAAACTGGGTGGGGTCACGGCCTCCTTCACTGCCTCCGTGGGGTCACTGTTCCTCACA  531
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Db   609  TTCAAACTGGGTGGGGTCACGGCCTCCTTCACTGCCTCCGTGGGGTCAGCTGTTCCTCACA  668

Qy   532  GCCATCGACAGGTACATATCCATTCACAGGCCCCTGGCCTATAAGAGGATTGTCACCAGG  591
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Qy   592  CCCAAGGCCGTGGTAGCGTTTTGCCTGATGTGGACCATAGCCATTGTGATCGCGGTGCTG  651
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Db   729  CCCAAGGCCGTGGTGGCCGTTTTGCCTGATGTGGACCATAGCCATTGTGATCGCGGTGCTG  788

Qy   652  CCTCTCCTGGGCTGGAACTGCGAGAAACTGCAATCTGTTTGCTCAGACATTTTCCCACAC  711
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   789  CCTCTCCTGGGCTGGAACTGCGAGAAACTGCAATCTGTTTGCTCAGACATTTTCCCACAC  848

Qy   712  ATTGATGAAACCTACCTGATGTTCTGGATCGGGGTCACCAGCGTACTGCTTCTGTTCATC  771
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Db   849  ATTGATGAAACCTACCTGATGTTCTGGATCGGGGTCACCAGCGTACTGCTTCTGTTCATC  908

Qy   772  GTGTATGCGTACATGTATATTCTCTGGAAGGCTCACAGCCACCCCGGTCCGCAATGATTCAG  831
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Db   909  GTGTATGCGTACATGTATATTCTCTGGAAGGCTCACAGCCACCCCGGTCCGCAATGATTCAG  968

Qy   832  CGTGGCACCCGAGAGAGCATCATCATCCACACGTCTGAGGATGGGAAGGTACAGGTGACC  891
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Qy   892  CGGCCAGACCAAGCCCGCATGGACATTAGGTTAGGTTAGCCAAGACCCTGGTCCTTGGGTG  951
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Db  1029  CGGCCAGACCAAGCCCGCATGGACATTAGGTTAGGTTAGCCAAGACCCTGGTCCTTGGGTG  1088

Qy   952  GTGTTGATCATCTGCTCTGGGGCCCCCTCTGCTTGCAATCATCAGGTGTATGAGGTCTTTGGGGAG  1011
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Db  1089  GTGTTGATCATCTGCTCTGGGGCCCCCTCTGCTTGCAATCATCAGGTGTATGAGGTCTTTGGGGAG  1148
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RESULT 12

LOCUS   CQ725118   1631 bp   DNA   linear   PAT 03-FEB-2004
DEFINITION Sequence 11052 from Patent WO2068579.
ACCESSION   CQ725118
VERSION   CQ725118.1 GI:42285975
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE   Kite, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 11052 06-SEP-2002;
            PE Corporation (NY) (US)
FEATURES   Location/Qualifiers
     source   1..1631
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                     /mol_type="unassigned DNA"
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ORIGIN

Query Match   95.3%; Score 1257.8; DB 2; Length 1631;
Best Local Similarity   99.4%; Pred. No. 0; Matches 1262; Conservative   0; Mismatches   7; Indels   0; Gaps   0;

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Qy   1149 ATGAACAAGCTCATTAAGACGGGTGTTTGCATTCTGCAGT 1208
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Db   352 CCTTCCTACCACTTCATCGGGCACCGTGGGCGG 411

Qy   1072 ACCGTGAACCCCATCATCTATGCTGCCACACGCCTTCCGGAGC 1131
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Db   515 CCTTCCTACCACTTCATCGGGCACCGTGGG 574

Qy   1209 ACCGTGAACCCCATCATCTATGCTGGCACACGCCTTCCGGAGC 1268
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Db   412 GTCTACAGCTTCATTGACTTCCAGTGTGTTCCACGTGTTTCTG 471

Qy   1132 ATGTTTCCCTCTTGTGTGAAGGGACACTGCGGGGAGA 1191
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Qy   1269 ATGTTTCCCTCTTGTGAAGGGCACTGCGGCGCGAGA 1328
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Qy   1192 TGCCTGCACAAACACGCAAACAATGCAGCCAGTTCACAGGGG 1251
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Qy   1329 TGCCTGCACAAACACGCAAACAATGCAGCCAGTTCACAGGGG 1388
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Qy   1252 AAGAGCACGGTCAAGATTGCCAAGGTAACCAAGTGTCTGTTCCACAGACAC 1311
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Qy   1312 GCTCTGTGA 1320
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RESULT 13

Qy   1012 ATGAACAAGCTCATTAAGACGGGTGTTTGCATTCTGCAGTATGCTCTGCCTGCTCGTGAACTCC 1131
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CS207294

LOCUS   CS207294   1755 bp   DNA   linear   PAT 08-DEC-2005
DEFINITION   Sequence 2 from Patent WO2005109000.
ACCESSION   CS207294
VERSION   CS207294.1 GI:83413202
KEYWORDS   .
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Hominidae; Homo.
REFERENCE   1
AUTHORS   Spittaels,K.F.
JOURNAL   Patent: WO 2005109000-A 2 17-NOV-2005;
               Galapagos Genomics N.V., (BE); Spittaels, Koenraad Frederick F. (BE)
FEATURES   Location/Qualifiers
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match   95.3%; Score 1257.8; DB 2; Length 1755;
Best Local Similarity   99.4%; Pred. No. 0; Mismatches   7; Indels   0; Gaps   0;
Matches 1262; Conservative   0;

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Qy        112 GTCCCAGCAGCAGCCAGGTGAACATTACAGAATTTACAACAAGTCTCTCTCGTCCTTCAAG 171
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Qy        172 GAGAATGAGGAGAACATCCAGTGTGGGGGAGAACTTCATGGACATAGAGTGTTTCATGGTC 231
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Db        419 GAGAATGAGGAGAACATCCAGTGTGGGGGAGAACTTCATGGACATAGAGTGTTTCATGGTC 478

Qy        232 CTGAACCCCAGCCAGCAGCTGGCCATTGCAGTCTTGTCTTGTCATCGCGGGGCCACCTTCACG 291
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Qy        292 GTCTCTGGAGAACCTCCTGGGTGTGCGGTCGTGTGCGGTCATCCTCCACTCCACGCCTGCGC 351
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Qy        352 CCTTCCTTACCACTTCATCGGCAGCCTGGCGCGGTGGCAGACCTCCTGGGGAGTTGTCATTTTT 411
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Qy        412 GTCTACAGCTTCATTGACTTCCACGTGTTCCACCGACAAAGATAGCCCGCAACGTGTTTCTG 471
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Qy        472 TTCAAACTGGGTGGGGTCACGCGCCTCCTTCACTGCTCCTCCGGTGGGGCAGCCGGCCTGGTCCTCACA 531
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Qy        532 GCCATCGACAGGTACATATCCATTCACAGGCCCCTGGGCCTATAAGGATGTTGTCACCAGG 591
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Qy        652 CCTCTCTTCTGGGCGTGGGGACTGCAGAGAAACTGCAAATCTGTTTGCTCAGACCATTTCCCACAC 711
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Db        899 CCTCTCCTGGGCGTGGGGACTGCAGAAACTGCAAATCTGTTTGCTCAGACCATTTTCCCACAC 958

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Db        959 ATTGATGAAAACCTACCTGAGTGTTCTGATGCGGAGTCACCAGCGGTACTGCCTTCAGTGCATC 1018
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RESULT 14
AX548798

LOCUS   AX548798   1755 bp   DNA   linear   PAT 26-NOV-2002
DEFINITION   Sequence 83 from Patent WO02061087.
ACCESSION   AX548798
VERSION   AX548798.1 GI:25813708
KEYWORDS   .
SOURCE   Homo sapiens (human)
ORGANISM   Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Hominidae; Homo.
REFERENCE   1
AUTHORS   Burmer,G.C., Roush,C.L. and Brown,J.P.
TITLE   Antigenic peptides, such as for G protein-coupled receptors
               (GPCR8), antibodies thereto, and systems for identifying such
               antigenic peptides
JOURNAL   Patent: WO 02061087-A 83 08-AUG-2002;
               Lifespan Biosciences, Inc. (US)
FEATURES   Location/Qualifiers
     source   1..1755
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Query Match   95.3%; Score 1257.8; DB 2; Length 1755;
Best Local Similarity   99.4%; Pred. No. 0; Mismatches   7; Indels   0; Gaps   0;
Matches 1262; Conservative   0;

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Qy         52 ACTGACCTCCTGGGAAGTCCCTTCCAAGAGAGAAGAGATGACTGCGGGGAGCAACCCCAGCTA 111
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Db    299 ACTTCCTTTAGGGAGGAAGTCCCTTCCAAGAGAAGATGACTTGCGGGAGACAAACCCCCAGCTA 358
Qy    112 GTCCCAGCAGACCAGGTGAACACATTACAGAATTTTACACAGAAGTCTCTTCGTCCTTCAAG    171
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Qy    292 GTCCTGGAGAACCTCCTGGTTGCTGTGGGCTCATCCTCCACTCACTCCTCCGCAGCCTCCGCAGG 351
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Qy    352 CCTTCCTACACCTTCATCGGCAGCCTGGCAGCCGTGGCAGACCTCCTGGGGAGTGTCATTTTT 411
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Db    599 CCTTCCTACACCTTCATCGGCAGCCTGGCAGCCGTGGCAGACCTCCTGGGGAGTGTCATTTTT 658
Qy    412 GTCTACAGCTTCATTGACTTCCACGTGTTCCACCGCAAAGATAGCCGCAACGTGTTTCTG    471
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Db    659 GTCTACAGCTTCATTGACTTCCACGTGTTCCACCGCAAAGATAGCCGCAACGTGTTTCTG    718
Qy    472 TTCAAACTGGGTGGGGTGACGGCCTCCTTCACTGCCTCCGTGGGCAGCCTGTTTCTCACA    531
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Db    719 TTCAAACTGGGTGGGGTGACGGCCTCCTTCACTGCCTCCGTGGGCAGCCTGTTTCTCACA    778
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Db    779 GCCATCGACAGGTACATCAGCATCCATTCACAGGCCCCCCTGGCCTATAAGAGGATTGTCACCAGG 838
Qy    592 CCCAAGGCCGTGGTAGCGTTTTGCCTGATGTGGACCATAGCCATTGTCATTGCCGTGCTG    651
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    839 CCCAAGGCCGTGGTAGCGTTTTGCCTGATGTGGACCATAGCCATTGTCATTGCCGTGCTG    898
Qy    652 CCTCTCCTCGGGTGGAACTGCGAGAAACTGCAATCGTGTTGCTCAGACATTTTCCCACAC    711
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Db    899 CCTCTCCTCGGGTGGAACTGCGAGAAACTGCAATCGTGTTGCTCAGACATTTTCCCACAC    958
Qy    712 ATTGATGAAAACCTACCTGATGTTCTGGAACTGGAGCGGGGGTCACCAGGTACTGCTTCTGTTCATC 771
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Qy    772 GTGTATCGGTACATGTATATTCTCTGGAAGGCTCACAGCCACGCCGTCCGCATGATCCAG    831
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Db   1019 GTGTATCGGTACATGTATATTCTCTGGAAGGCTCACAGCCACGCCGTCCGCATGATCCAG    1078
Qy    832 CGTGGGCACCCAGAAGAGCATCATCATCCACAGTCTCCGAGGAGTGGAAGGTACAGGTGACC 891
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Qy    892 CGGCCAGACCAAGCCCGGCCACCTGGCCATGGACATTAGGTTAGCCAAGACCCTGGTCCTGGTG 951
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Db   1139 CGGCCAGACCAAGCCCGGCCACCTGGCCATTGGACATTAGGTTAGCCAAGACCCTGGTCCTGGTG 1198
Qy    952 GTGTTGATCATCTGCTGGGGCCCTCTGCTTGCAATCATGGTGTATGATGTGTTCGGGAAG    1011
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Db   1199 GTGTTGATCATCTGCTGGGGCCCTCTGCTTGCAATCATGGTGTATGATGTCTTTGGGAAG    1258
Qy   1012 ATGAACAAGCTCATTAAGACGGTGTTTGCATTCTGCAGTATGCTCTGCCTGCTGAACTCC    1071
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Db   1259 ATGAACAAGCTCATTAAGACGGTGTTTGCATTCTGCAGTATGCTCTGCCTGCTGAACTCC    1318
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ACCESSION   X54937
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SOURCE      Homo sapiens (human)
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            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Gerard,C., Mollereau,C., Vassart,G. and Parmentier,M.
  TITLE     Nucleotide sequence of a human cannabinoid receptor cDNA
  JOURNAL   Nucleic Acids Res. 18 (23), 7142 (1990)
  PUBMED    2263478
REFERENCE   2  (bases 1 to 1755)
  AUTHORS   Gerard,C.M., Mollereau,C., Vassart,G. and Parmentier,M.
  TITLE     Molecular cloning of a human cannabinoid receptor which is also
            expressed in testis
  JOURNAL   Biochem. J. 279 (Pt 1), 129-134 (1991)
  PUBMED    1718258
REFERENCE   3  (bases 1 to 1755)
  AUTHORS   Gerard,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-OCT-1990) Gerard C., IRIBHN, Campus Erasme, 808 v De
            Lennik, 1070 Bruxelles, Belgium
COMMENT     Data kindly reviewed (14-MAR-1991) by Gerard C.
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OM nucleic - nucleic search, using sw model

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

Run on: June 16, 2006, 23:52:42 ; Search time 69 Seconds
(without alignments)
4503.089 Million cell updates/sec

Title: US-10-521-428A-1
Perfect score: 1320
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Minimum DB seq length: 0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1320	100.0	1320	6	US-10-521-428A-1	Sequence 1, Appli
2	245.2	18.6	1083	7	US-11-242-505A-1	Sequence 2, Appli
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4	60.8	4.6	1885	7	US-11-289-102-47	Sequence 47, Appl
5	56.8	4.1	1080	7	US-11-257-851A-74	Sequence 74, Appl
6	53.6	4.1	599	6	US-10-488-619-1656	Sequence 1656, Ap
7	53	4.0	1074	7	US-11-302-678-39	Sequence 39, Appl
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11	49.6	3.8	1650	7	US-11-312-958-39	Sequence 39, Appl
12	49.4	3.7	5132	6	US-10-505-928-663	Sequence 663, App
13	48.2	3.7	2193	6	US-10-504-973-47	Sequence 47, Appl
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34	40.6	3.1	1152	6	US-10-449-902-35	Sequence 35, Appl
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45	39.4	3.0	1005	6	US-10-449-902-22331	Sequence 22331, A

ALIGNMENTS

RESULT 1
US-10-521-428A-1

; Sequence 1, Application US/10521428A
; Publication No. US20060115816A1
; GENERAL INFORMATION:
; APPLICANT: Vu, Huy Khang
; APPLICANT: Groblewski, Thierry
; APPLICANT: Greasley, Peter
; TITLE OF INVENTION: Splice Variant Cannabinoid Receptor (CB1B)
; FILE REFERENCE: A5ZD-P01-750
; CURRENT APPLICATION NUMBER: US/10/521,428A
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 0202240-8
; PRIOR FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1 :
; LENGTH: 1320
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-521-428A-1

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RESULT 3
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; Publication No. US20060099656A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Healy, Aileen
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
; FILE REFERENCE: MPI2001-288PIRCPIOMNIM
; TITLE OF INVENTION: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,
; CURRENT APPLICATION NUMBER: US/11/242,505A
; CURRENT FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US 10/290,078
; PRIOR APPLICATION NUMBER: US 10/290,078
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/347,949
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 10/320,351
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,606
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1790
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-242-505A-1

Query Match   18.6%; Score 245.2; DB 7; Length 1790;
Best Local Similarity   55.9%; Pred. No. 3.2e-58;
Matches 537; Conservative 0; Mismatches 378; Indels 45; Gaps 2;

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Qy   887 TGACCCGGCCCAGACCAAGCCCGCATTGGACATTAGGTTAGCCAAGACCCTTGGTCCTTGATCC 946
          ||||||| |||| || |||| |||||||| |||| |||| ||| | ||
Db   692 TGGCCAGGAAGTGGCCCGGAATGAGCGGTGGATTGAGTGTGAGGTTGGCCAAGACCCTAGGGCTAGTGT 751

Qy   947 TGGTGGTGTTGATCATCTGCTGGGGGGCCCTCTGCTTGCAAATCATGGTGTHATGATGTCTTTG 1006
          |||| || |||| || | |||||| | || | |||||| | | |||||| || |
Db   752 TGGCTGTGCTCCTCATCTGTTGGTTGGTTCCCAGCTGCGGCCCTCATGGCCTGGGGGTGT 811

Qy   1007 GGAAGATGAACAAGCTCATTAAGACGGGTGTTTGCATTCTGCAGTATGTGCTTGCCTGCTGA 1066
          | ||||| | |||| | | ||| | || || |||||||| | | | ||| |||
Db   812 CTTACGCTCAGTGACCAGTCAAGAAAGGCCTTTGCTTTGCGTGCGTCATGCTGTGCGCTCATCA 871

Qy   1067 ACTCCACCGTGAACCCATCATCATCTATGCTCTGAGGAGTAAGGACCTGGCCG 1126
          ||||| | |||||| | ||| || | || |||||| ||| || ||
Db   872 ACTCCATCGTCAACCCTGTCATCTATGCTCTACGGAGTGGGAAGAGGATCCGCTTCCTCTCTGCCC 931

RESULT 4
US-11-289-102-47
; Sequence 47, Application US/11289102
; Publication No. US20060121511A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Hyerim
; APPLICANT: Shaw, Peter M.
; APPLICANT: Clark, Edwin
; TITLE OF INVENTION: BIOMARKERS AND METHODS FOR DETERMINING SENSITIVITY TO
; TITLE OF INVENTION: MICROTUBULE-STABILIZING AGENTS
; FILE REFERENCE: 10338 NP
; CURRENT APPLICATION NUMBER: US/11/289,102
; CURRENT FILING DATE: 2005-11-29
; PRIOR APPLICATION NUMBER: US 60/631,993
; PRIOR FILING DATE: 2004-11-30
; NUMBER OF SEQ ID NOS: 395
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 47
; LENGTH: 1885
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-289-102-47

Query Match   4.6%; Score 60.8; DB 7; Length 1885;
Best Local Similarity   49.5%; Pred. No. 3.1e-07;
Matches 186; Conservative 0; Mismatches 187; Indels 3; Gaps 1;

Db   383 TCTTTGCATGCAGCTTTGTTGTGAATTTCCATGTTTTCCATGTGTGTGGGATTCAAAGGGCTGCT 442

Qy   467 TTCTGTTCAAACTGGGGTGGGGGTCACGGCGCTCCTTCACTGCGCTCCGTGTGGGGCAGGCTGTTCC 526
          ||||||
Db   443 TCCTTCCTGAAGATTGGCCAGCGTGACTAATGAGACCTTCACAGCCTCTGTGGGGTAGCCTTCCTGC 502

Qy   527 TCACAGCCATCGACAGAGGTACATATACCATTCACAGCCCCTGGGCCTATAGAGGATTGTCA 586
          ||| ||||| | ||| ||| ||
Db   503 TGACCCGCCATTGACCGATACCTCTCCCTGGGCTATCCAACCTTCCTACAAAGCTCTCTCA 562

Qy   587 CCAGGCCCAAGGCCGTGGTAGGCGTTTGCCTGATGTGGACCATAGCCATTGTGATCGCCG 646
          |||||| | || ||| || || | ||| || |||||| | ||| ||| |||
Db   563 CCCGTGGAAGGGCACTGGTTGACCCTGGGCATCAGTGGGGTCCTCTCAGCAACTAGTCTCT 622

Qy   647 TGCTGCCTCTCCTGGGCTGGAACTGCCGAGAAACTGCAATCTGTTTGCTCAGACATTTTCC 706
          ||| ||| | |||||| | || || ||| | | || | | | |||||
Db   623 ACCTTGCCCCTTCATGGGATGGAACTTGCTGTCCAGGC--------CCTGGCTCTGAGCTTTTCC 676

Qy   707 CACACATTGATTGAAAACCTACCCTGATTGTTCTTGGATTCGGGGGGTCACCGGCTACTGCTTCTGT 766
          ||||| ||| | | ||| || || |||| |||| |||| | ||| || || |
Db   677 CACTGATCCCAATCACTACCTGCTGAGCTGGCTCCTGTTCATGGCCTTCCTCTTTTCCG 736

Qy   767 TCATCGTGTATGCGTACAACATGTATATATTCTTCTGGAAGGCTCACAGCCACGCCGTTCCGCATGA 826
          ||||| || ||||| | ||| | | |||||||||||||||||||||||||||||||||
Db   737 GAATCATCTACACCTTATGGGCCATTGTTCTCTTCTGGAAGAGGCCCATCACAGCATGTGGCCAGCTT-- 794

Qy   827 TTCACGGTGGCACCCAGAGAGAGAGCATCATCATCCACACGTCTGAGGATGGGAAGGTTACAGG 886
                                                    |||||||||||||||||||||||
Db   795 --------------------------------------GTCTGGCCACCAGGACAGGCAGG 817

Qy   887 TGACCCGGCCCAGACCAAGCCCGCATTGGACATTAGGTTAGCCAAGACCCTTGGTCCTTGATCC 946
          ||||||| |||| || |||| |||||||| |||| |||| ||| | ||
Db   818 TGCCAGGAATGAGCGGTGGATTGAGTGTGAGGTTGGCCAAGACCCTAGGGCTAGTGT 877

Qy   947 TGGTGGTGTTGATCATCTGCTGGGGGGCCCTCTGCTTGCAATCATGGTGTATGATGTCTTTG 1006
          |||| || |||| || | |||||| | || | |||||| | | |||||| || |
Db   938 TGGCTGTGCTCCTCATCTGTTGGTTGGTTCCCAGCTGCGGCCCTCATGGCCTGGGGGTGT 997

Qy   1007 GGAAGATGAACAAGCTCATTAAGACGGGTGTTTGCATTCTGCAGTATGTGCTTGCCTGCTGA 1066
          | ||||| | |||| | | ||| | || || |||||||| | | | ||| |||
Db   878 TGGCTGTGCTCCTCATCTGTTGGTTGGTTCCCAGCTGCGGCCCTCATGGCCTGGGGGTGT 937

Qy   1067 ACTCCACCGTGAACCCATCATCATCTATGCTCTGAGGAGTAAGGACCTGGCCG 1126
          ||||| | |||||| | ||| || | || |||||| ||| || ||
Db   998 ACTCCATCGTCAACCCTGTCATCTATGCTCTACGGAGTGGGAAGAGGATCCGCTTCCTCTCTGCCC 1057

Qy   167 TCAAGGAGAATGAGGAGAACATCCAGTGTGGGGAGAACTTCATGGACATAGAGTGTTTCA 226
          ||||| ||| || | | || ||| |||| ||| || ||| || |||| ||
Db   143 TGACAGAGATAGCCAATGGCTCCAAGGAATGGCTTGGATTCCAAACCCTATGAAGGATTACA 202

Qy   227 TGGTCCTGAACCCCAGCAGCAGCTGGCCATTGCAGTCTGTGTCCTCACGCTGGGCACCT 286
          ||| ||||| || ||| || | || | | | | | || | ||| || |||
Db   203 TGATCCTGAGTGGTCCCCAGAGAACAGCTGTTGCTGCGTTTGTCGTTCTGGGCCTGC 262

Qy   287 TCACGGTCCTTGGAGAACCTCTGTTGTGCGTCATCCTCCACTCCCGCAGCCTCCGGCT 346
          | || | || | |||| || | | | || | || ||| || | | ||||
Db   263 TAAGTGCCTGGAGAACTGGGTGCTCTATCTGATCGTCCTCCCACCAACTCCCC 322

Qy   347 GCAGGCCTTCCTACCACTTCATCGTGGCGTGTGCCTGGGCGGTGGCAGACCTGGTGTGTCA 406
          ||||| ||||| | || | || | | ||| || ||||| | | |||| | || |
Db   323 GGAAGCCCTCATACCTGTTCAATACCTTGAGCTTGCCTTGGGGGCTGAAAGATAGCCGCAAACGTGT 382

Qy   407 TTTTGTTCTACAGCTTCATTGACTTCCACGTGTTCCACCGCAAAGATAGCCGCAAACGTGT 466
          |||| |||| | | | | | || | | || || || | |||| | ||||||||
Db   407 TTTTGTTCTACAGCTTCATTGACTTCCACGTGTTCCACCGCAAAGATAGCCGCAAACGTGT 466

RESULT 5

US-11-257-851A-74
Sequence 74, Application US/11257851A
Publication No. US20060105951A1
GENERAL INFORMATION:
;   APPLICANT: Cunningham, Mark
;   APPLICANT: Stojanovic-Susulic, Vedrana
;   APPLICANT: O'Neil, Karyn
;   APPLICANT: Huang, Chichi
;   APPLICANT: Luo, Jeffrey
;   TITLE OF INVENTION: Melanocortin Receptor Binding Mimetibodies, Compositions, Methods
;   FILE REFERENCE: CEN5080 USA NP
;   CURRENT APPLICATION NUMBER: US/11/257,851A
;   CURRENT FILING DATE: 2005-10-25
;   PRIOR APPLICATION NUMBER: 60/621,960
;   PRIOR FILING DATE: 2004-10-25
;   NUMBER OF SEQ ID NOS: 85
;   SOFTWARE: Patentin version 3.2
;   SEQ ID NO 74
;   LENGTH: 1080
;   TYPE: DNA
;   ORGANISM: Homo sapiens

US-11-257-851A-74

Query Match   4.3%;   Score 56.8;   DB 7;   Length 1080;
Best Local Similarity   50.0%;
Matches 216;   Conservative   0;   Mismatches 192;   Indels   24;   Gaps   2;

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Qy  296  TGGGAGAACCTCCTGGTGTGCGTTGCGGTCATCCTCCACTCCGCAGCCTCCGGCTGCAGGGCTT  355
Db  397  TGGGCGGGCAACCTGCTGTGTGCGCCCGGGTGGGCAACACTCTGGATGCAGGCCCA          456
Qy  356  CCTACCACTTCATCGGGCAGAGCCTGGGGGTGGCAGAGACCTTCCTGGGGGAGTGTGCATTTTTGTGTCT  415
Db  457  CCAACTACTTCCTGGTGTCCCTGGGCTTGGGGGCCCAGAGCTGGGGGGCTCTTGGCCATCC          516
Qy  416  ACAGCTTCATTGACTTCACGTGTTCCACCGTGTTCCACCGCAAAGATAGACGCGAAGGTGTTTCTGTTCA  475
Db  517  CCTTTTGCCATCACCATCAGCCTGGGCTTCAGCTGCGA---CTTCTACGGCTGCCTCTTCC          573
Qy  476  AACTGGGTGGGGGTCACGGACGGTCCACTCCTTCACTCCGTGGGCAGCCTGTTCCTTCACAGCCA          535
Db  574  TCGCCTTGCTTGCTGCTGGTGCTCACGGACGGGAGCGCTGCCATCTTCAGCCTTTCAGTTGCGGTCACAGGA  633
Qy  536  TCGACAGGTACATATCATTCACAGGCCCCTGGCCTATAAGAGGATTATTCTCTCACCTGGCCCA          595
Db  634  TCGACAGGATTACCTGGCCGTTTTGCCTGAGTGTGGACCATAGCCATTGTGATGCCGGTGCTGCTC          693
Qy  596  AGGCCGTGGTAGCGTTTTGCCTGATGTGGACACATAGCCATTGTGATGCCGGTGCTGCTC          655
Db  694  GAGCAAGAGAGGGGTCATTGCTGCTGTCCTCTGGGGTCCTTGCCTTTGCATCGATCGATTGACTCCAT  753
Qy  656  TCCTGGGCTGGAACTG  671
Db  754  TCCTGGGGTGGAACAG  769
```

RESULT 6

US-10-488-619-1656
Sequence 1656, Application US/10488619
Publication No. US20060099578A1
GENERAL INFORMATION:
;   APPLICANT: Greenlee, Winner and Sullivan, P.C.
;   TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
;   TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
;   FILE REFERENCE: 98-01 WO
;   CURRENT APPLICATION NUMBER: US/10/488,619
;   CURRENT FILING DATE: 2004-03-01
;   NUMBER OF SEQ ID NOS: 3040
;   SOFTWARE: Patentin version 3.1
;   SEQ ID NO 1656
;   LENGTH: 599
;   TYPE: DNA
;   ORGANISM: Mus musculus

US-10-488-619-1656

Query Match   4.1%;   Score 53.6;   DB 6;   Length 599;
Best Local Similarity   51.7%;
Matches 122;   Conservative   0;   Mismatches 114;   Indels   0;   Gaps   0;

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Qy  601  GTGGTAGGGTTTTGCCTGATGTGGACCATAGCCATTGTGATGCCGGTGCTGCTCCTGG      660
Db   30  GTGGTGGTGCATTGTTAGTCATCTGGACTATGGCCATCTGTGATGGCGGGCTGTATACCCAGTGTTG      89
Qy  661  GGCTGGAACTGCCGAGAAACTGCAAATCTGTTGTTGCTCAGACATTTTCCCACACATTGATGATGAA     720
Db   90  GGCTGGAACTGCATCGTGATAGTCAGCTCCAACACATTGCCACCCTCTACAGTGAC             149
Qy  721  ACCTACCTGATGTTCTGATCGGGGTCACCAGCGTACTGCTTCGTTCATGTGTATGCG             780
Db  150  TCCTTACTTAGTCTTCTGGGCCCATTTTCAACCTGGTGCATTGGTGGTTCTC                209
Qy  781  TACATGTATATTCTCTGGAAAGGCTCACAGCCACGCCCGCGTCCGCATGATTCAGGGTGG          836
Db  210  TACCCTCACATCTTTGGCTCATGGTTCGGCCAGAGGACTATGAGAGGATGGTCCGGGCATAG        265
```

RESULT 7

US-11-302-678-39
Sequence 39, Application US/11302678
Publication No. US20060088881A1
GENERAL INFORMATION:
;   APPLICANT: Millennium Pharmaceuticals, Inc.
;   APPLICANT: Silos-Santiago, Inmaculada
;   APPLICANT: Venkateswarlu, Karicheti
;   TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
;   TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 641, 260, 55089, 21407, 42032, 46656, 62553,
;   TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
;   FILE REFERENCE: MP102-012PIRNM OMNI
;   CURRENT APPLICATION NUMBER: US/11/302,678

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Qy  266  TGTCCCTCACGGCTGGGCAACCTTCACGGTCCTCGGAGAACCTCTGGTCTGTGGTCATCC       325
Db  242  TTTTCCTCGTCTCCTGCTGGGCCATCGTCAGTCTGCTCTGGGCATCGTTGTATCCTGGGT       301
Qy  326  TCCACTCCCGCGAGCCCTCCGCGTGCAGGCCTTCCTACCACTTCATCGGGCAGAGCCTGGGGGTGG       385
Db  302  TCAGGAACGGCAACCTGCACTCC---CCGATGTACTCTTTCTCTGCAGCCTGGCGGTGG         358
Qy  386  CAGAGACCTTCCTGGGGGAGTC-----------TCATTTTTGTCTACAGCTTCA        424
Db  359  CCGACAGTGCTGGTAAGTGTGTCCAAATGCCCTGGAGACCATCATGATACGGCCATCACA        418
Qy  425  TTGACTTCACGTGTTCCACCGCAAAGATAGCCGACAAGTGTGTTTCTGTTCAAACTGGGTG       484
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; CURRENT FILING DATE:                  2005-12-14
; PRIOR APPLICATION NUMBER:             US/10/345,680
; PRIOR FILING DATE:                    2003-01-16
; PRIOR APPLICATION NUMBER:             US 60/349,511
; PRIOR FILING DATE:                    2002-01-18
; PRIOR APPLICATION NUMBER:             US 60/360,500
; PRIOR FILING DATE:                    2002-02-28
; PRIOR APPLICATION NUMBER:             US 60/365,041
; PRIOR FILING DATE:                    2002-03-15
; PRIOR APPLICATION NUMBER:             US 60/374,063
; PRIOR FILING DATE:                    2002-04-19
; PRIOR APPLICATION NUMBER:             US 60/403,468
; PRIOR FILING DATE:                    2002-08-14
; PRIOR APPLICATION NUMBER:             US 60/414,262
; PRIOR FILING DATE:                    2002-09-27
; PRIOR APPLICATION NUMBER:             US 60/419,986
; PRIOR FILING DATE:                    2002-10-21
; PRIOR APPLICATION NUMBER:             US 60/423,809
; PRIOR FILING DATE:                    2002-11-05
; PRIOR APPLICATION NUMBER:             US 60/429,797
; PRIOR FILING DATE:                    2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 39
  LENGTH: 1074
  TYPE: DNA
  ORGANISM: Homo Sapiens
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (1)...(1074)
; US-11-302-678-39

Query Match       4.0%;     Score 53;   DB 7;   Length 1074;
Best Local Similarity   44.8%;   Pred. No. 3.4e-05;
Matches  246;  Conservative    0;  Mismatches  300;  Indels    3;  Gaps    1;

Qy    277 CTGGGCACCTTCACGGTCCTGGAGAAACCTCTGTGGTGCTGTGGCGTCATCCTTCCACTCCCGC 336
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    148 CTGGTGGGCGGCGACGTTCGCCTGGAACCTGCTGCTGGGCGACCATCCTCCGTGTACGC 207

Qy    337 AGCCTCCGCGTGCAGGCCTTCCTACCACTTCATCGGCAGCCTGGGCGGTGGCGAGAGACCTCCTG 396
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    208 ACCTTCCACGCGCGTGCCCCACAACCTTGGTGGCATCCATAGGCCGTTCTCGGANGTCCTGGTG 267

Qy    397 ---GGGAGTGTCATTTTTGTTCTACAGCTTCATTGACTTCCACCGTGTTCCACCGCAAAAGAT 453
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    268 GCCGCGCTGGTCATGCCGCCTGAGCCTGGTGCATGAGCGTGCCGCGCTGGCAGCTA 327

Qy    454 AGCCGCAACGTGTTTCTGTTCAAAACTCGGGTGGGGGGTCACGGGCTTCCTTCACTGCCTCCGTG 513
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    328 GGTCGGAGCTGTTGCCACGCTTTGGATCCGTGCGACGTGCTTTGCTGCACGCCAGCATC 387

Qy    514 GGCAGCCTGGTTCCTTCACAGCCATCGACAGGTACATATCCATTCACAGCCCCTGGCCTAT 573
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    388 TGGAACGTGACGGCCATAGCCCTGGACCGGCTACTGCTCGTCATCACGGCCACATGGAATAC 447

Qy    574 AAGAGGATTGTCACCAGCCCAAGGCCCTGTGGTAGGGTTTTGCCTGAGTGGACCATAGCC 633
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    448 ACGCTCCGCACCCGAGTGCGTCTCCAAGTGCATGATCGGCGCTCACCTGGGCACTCTCC 507

Qy    634 ATTGTGATCGCGCGCGTGCCTCTCGGGCTCGGAGAAACTGCAGAAACTGCAATCTGTTTGC 693
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    508 GCTGTCATCCTGCTGCCCCGCTGCTTTTTGGCTGGGAGACGTACTCTGAGGGCAGC 567

Qy    694 TCAGACATTTTCCCACACATTGATGAAAACCTACCTGATGTTCGGATCGGGGTCACCAGC 753
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    568 GAGGAGTGCCAGGTAAGCGGCGAGCCTTCCTACGCCGTCTTCCACGGTAGGCGCCTTC 627

Qy    754 GTACTGCTTCTGTTCATCGTGTATGCGTACATGTATATTCTCTGGAAGGCTCACAGCCAC 813
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    628 TACCTGCCGCCTGTGTGGTGGCTTCTTCGTGTACTGGAAGAGATCTACAAGGCTGCCAAGTTC 687

Qy    814 GCCGTTCCGC 822
          ||||||||||
Db    814 CGCGTGGGC 822
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Db    688 CGCGTGGGC 696
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US-11-302-678-37
; Sequence 37, Application US/11302678
; Publication No. US20060088881A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Inmaculada
; APPLICANT: Venkatesswarlu, Kericheti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656,
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318,
; FILE REFERENCE: MPI02-012P1RNM_OMNI
; CURRENT APPLICATION NUMBER: US/11/302,678
; CURRENT FILING DATE:                  2005-12-14
; PRIOR APPLICATION NUMBER:             US/10/345,680
; PRIOR FILING DATE:                    2003-01-16
; PRIOR APPLICATION NUMBER:             US 60/349,511
; PRIOR FILING DATE:                    2002-01-18
; PRIOR APPLICATION NUMBER:             US 60/360,500
; PRIOR FILING DATE:                    2002-02-28
; PRIOR APPLICATION NUMBER:             US 60/365,041
; PRIOR FILING DATE:                    2002-03-15
; PRIOR APPLICATION NUMBER:             US 60/374,063
; PRIOR FILING DATE:                    2002-04-19
; PRIOR APPLICATION NUMBER:             US 60/403,468
; PRIOR FILING DATE:                    2002-08-14
; PRIOR APPLICATION NUMBER:             US 60/414,262
; PRIOR FILING DATE:                    2002-09-27
; PRIOR APPLICATION NUMBER:             US 60/419,986
; PRIOR FILING DATE:                    2002-10-21
; PRIOR APPLICATION NUMBER:             US 60/423,809
; PRIOR FILING DATE:                    2002-11-05
; PRIOR APPLICATION NUMBER:             US 60/429,797
; PRIOR FILING DATE:                    2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 37
  LENGTH: 1159
  TYPE: DNA
  ORGANISM: Homo Sapiens
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (64)...(1137)
; US-11-302-678-37

Query Match       4.0%;     Score 53;   DB 7;   Length 1159;
Best Local Similarity   44.8%;   Pred. No. 3.5e-05;
Matches  246;  Conservative    0;  Mismatches  300;  Indels    3;  Gaps    1;

Qy    277 CTGGGCACCTTCACGGTCCTGGAGAAACCTCTGTGGTGCTGTGGCGTCATCCTTCCACTCCCGC 336
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    211 CTGGTGGCGGCGACGTTCGCCTGACCTGCTGCTGGGCGACCATCCTCCGTGTACGC 270

Qy    337 AGCCTCCGCGTGCAGGCCTTCCTACCACTTCATCGGCAGCCTGGGCGGTGGCGAGAGACCTCCTG 396
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    271 ACCTTCCACGCGCGTGCCCCACAACCTTGGTGGCATCCATAGGCCGTTCTCGGANGTCCTGGTG 330

Qy    397 ---GGGAGTGTCATTTTTGTCTACAGCTTCATTGACTTCCACCGTGTTCCACCGCAAAAGAT 453
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    331 GCCGCGCTGGTCATGCCGCCTGAGCCTGGTGCATGAGCGTGCCGCGCTGGCAGCTA 390

Qy    454 AGCCGCAACGTGTTTCTGTTCAAAACTCGGGTGGGGGGTCACGGGCTTCCTTCACTGCCTCCGTG 513
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    391 GGTCGGAGCTGTTGCCAGCTTTGGATCGGCGACGTGCTTTGCTGCACGGCACAGCATC 450

Qy    514 GGCAGCCTGGTTCCTCACAGCCATCGACAGGTACATATCCATTCACAGCCCCTGGCCTAT 573
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    451 TGGAACGTGACGGCCATAGCCCTGGACCGGCTACTGCTCGTCATCACGGCCACATGGAATAC 510
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RESULT 9
US-11-257-851A-78
; Sequence 78, Application US/11257851A
; Publication No. US20060105951A1
; GENERAL INFORMATION:
; APPLICANT: Cunningham, Mark
; APPLICANT: Stojanovic-Susulic, Vedrana
; APPLICANT: O'Neil, Karyn
; APPLICANT: Huang, Chichi
; APPLICANT: Luo, Jeffrey
; TITLE OF INVENTION: Melanocortin Receptor Binding Mimetibodies, Compositions, Methods
; TITLE OF INVENTION: Uses
; FILE REFERENCE: CEN5080 USA NP
; CURRENT APPLICATION NUMBER: US/11/257,851A
; CURRENT FILING DATE: 2005-10-25
; PRIOR APPLICATION NUMBER: 60/621,960
; PRIOR FILING DATE: 2004-10-25
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 78
; LENGTH: 975
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-257-851A-78

Query Match   3.8%;   Score 49.6;   DB 7;   Length 975;
Best Local Similarity   58.2%;   Pred. No. 0.00028;
Matches   107;   Conservative   0;   Mismatches   74;   Indels   3;   Gaps   1;

Qy   574 AAGAGGGATTGTCACCAGGCCCAAGGCCGTGGTAGGCGTTTTGCCTGAIGTGGACCATAGCC 633
Db   511 ACGCTCCGCACCGCAAGTGCGTGTCTCCAACGTCATGATCGCGGCTCACCTGCCACTCTCC 570

Qy   634 ATTGTGATCGCGCCGTGCTCCCTCTCCTGGGCTGGGAACTGCGCAGAAACTCAATCTGTTTGC 693
Db   571 GCTGTCATCCTTCTCTGGCCCCCGCCCGGTGCTTTTTGGCGTGGGGGAGAGACGTACTCTGAGGGGCAGC 630

Qy   694 TCAGACAITTCCCACACATTGATGAAACCTACCTACTTCGTTCTGGATGGGGGTCACCAGC 753
Db   631 GAGGAGTGCCAGTAAGCGCCGGAGCCCTTCCTACGCCGTGTTCTTCCACCGTAGGCGCCTTC 690

Qy   754 GTACTGCTTCTGTTCATCGTGTATATATTCTGGAAGGCTCACAGCCAC 813
Db   691 TACCTGCCGCTCTGTGTGGGTGCTCTTCGTTACTGTGAGATCTCACAAGGCTGCCAAGTTC 750

Qy   814 GCCGTCCGC 822
Db   751 CGCGTGGGC 759

RESULT 11
US-11-312-958-39
; Sequence 39, Application US/11312958
; Publication No. US20060100152A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Rosenfeld, Julie Beth
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,
; TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,
; TITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,
; TITLE OF INVENTION: 95431, 22245, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR
; TITLE OF INVENTION: 13424 MOLECULES
; FILE REFERENCE: MP102-027P1RNOMNIM
; CURRENT APPLICATION NUMBER: US/11/312,958
; CURRENT FILING DATE: 2005-12-20

RESULT 10
US-10-449-902-19945
; Sequence 19945, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 19945
; LENGTH: 1579
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK070284
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-19945

Query Match   3.8%;   Score 49.6;   DB 6;   Length 1579;
Best Local Similarity   47.4%;   Pred. No. 0.00036;
Matches   182;   Conservative   0;   Mismatches   199;   Indels   3;   Gaps   1;

Qy   82 AAGATGACTGCGCGGAGACAAACCCCCAGCTAGTCCCAGCAGACCAGGTGAACATTACAGAA 141
Db   682 AATGTGACCATCAGCGGCCATCACCATTCTTAGCCACCTTCAAACTCGCCCAACACCGATGGA 741

Qy   142 TTTTTACACAAGTCTCTCTCGTCCTTCAAGGAGGAATGAGGAGAACATTCCAGTGTGGGGAG 201
Db   742 ATCGACCCAGATTCTTCCTCCCAITGTCAAGATCAGAGGACAGCTACATCGTGTCCGGCGAC 801

Qy   202 AACTTCATGGACAATAGAGTGTTTCATGGTCCTGAAACCCAGCCAG---CAGCTGGCCATT 258
Db   802 GACTGCATCGCCCGTGAAGAGCGGCTGGGACCAGTACGGCCATCAAGTTCAACATGCCGAGC 861

Qy   259 GCAGTCCTGTCCCTCACCCTGGGCACCCTTCACGGTCCTCGGAGAACCTCCTCGTGCTGTGC 318
Db   862 CAGCACATCCTCATCAGGAGAGGCCTCACCTGCATCTCCCCGACGAGCGCCATGATCGGCTC 921

Qy   319 GTCATCCTCCACTCCCGAGCCTCCGTGCAGGCGTTCCTACCACTTCATCGGGCGGCCTG 378
Db   922 GGCAGCGGAGATGTCCGGCGGCATCCGCGAGCGCGCGCCGGGCCGCAACGTCGCCATCGAC 981

Qy   379 GCCGTGGCGCAGACCCTCCTGGGGAGTGTCATTTTTGTCTACAGCTTCATTGACTTCCACGTG 438
Db   982 ACCGAGTCGGCCCGTCAGGATCAAGTCCGGCGTGGGCGGCGGCGCTACGTCAAGGACGTG 1041

Qy   439 TTCCACCGCAAAGATAGCCGCGAAC 462
Db 1042 TTCGTCCGGGGCCTCAGCCTCCAC 1065

; PRIOR APPLICATION NUMBER: US/10/369,022
; PRIOR FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: US 60/360,495
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/370,121
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/373,010
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/373,908
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/377,717
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US 60/379,949
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/382,409
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/385,280
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/386,879
; PRIOR FILING DATE: 2002-06-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 39
; LENGTH: 1650
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (616)...(1593)
US-11-312-958-39

Query Match   3.8%; Score 49.6; DB 7; Length 1650;
Best Local Similarity   58.2%; Pred. No. 0.00037;
Matches 107; Conservative   0; Mismatches 74; Indels   3; Gaps   1;

Qy   266 TGTCCCTTCACGCTGGGGCACCTTCACGGTTCCTGGAGAACCTCCTGGTGCTGCGTCATCC 325
               ||||||||||| ||| || |||| ||||||| |||| ||||||||||||||||
Db   740 TGTTTCTCACTCTGGGGTCTCATCAGCCCTCTTGGAGAACATCTTGGTCATAGGGGGCCATAG 799

Qy   326 TCCACTCCCGCAGCCTCCGCTGCAGGCCCTTCCTACCACTTCATCGGCAGCCTCGCGGTGG 385
               || | || |||||| | ||||| ||||| ||||||||||||||||||||
Db   800 TGAAGAACAAAAAACCTGCACTCC---CCCATGTACTTCTTCGTGTGTGCAGCCTTGGCAGTGG 856

Qy   386 CAGACCTTCCTGGGGGAGTGTCATTTTTTGTCTACAGCTTCATTGACTTCACGTGTTCCACC 445
               |||| |||||||||| |||| |||||||||||| ||||||||| ||||||| |||
Db   857 CGGACATGCCTGGTGAGCANGTCCNGGGAGGACCATCACCATCTACCTACTCAACA 916

Qy   446 GCAA 449
               |||
Db   917 ACAA 920

Query Match   3.7%; Score 49.4; DB 6; Length 5132;
Best Local Similarity   51.1%; Pred. No. 0.00074;
Matches 116; Conservative   0; Mismatches 111; Indels   0; Gaps   0;

Qy   259 GCAGTCCTGTCCCTCACGCTGGGGCACCTTCACGGTTCCTGGAGAACCTCCTGGTGCTGC 318
               ||||| | || ||| ||||| ||||| ||||||| ||||||||| | |||||| |
Db   2126 GAAGTCCTTCGTTCCTCCGCGCGCCCAGGGCCCCATTCCAGAGCCAGGGCTCCTGGAGAAGTG 2067

Qy   319 GTCATCCTCCACTCCCGCAGCCTCCGCTGCAGGCCCTTCCTACCACTTCATCGGCAGCCTG 378
               ||| ||||| || ||||| || ||| ||||| ||||| ||||||||||||||||||
Db   2066 ATCCTCCCTCTTCCTCCCTCCCTGGCCTTCTCCCCCTGGCCTCCCTCCCTCCCTCCACGTC 2007

Qy   379 GCGGTGGCAGACCTTCCTGGGGGAGTGTCATTTTTGTCTACAGCTTCATTGACTTCACGTG 438
               || |||||| |||| ||||||||||||| |||||||||||||||||||||||||||
Db   2006 TGGGGCGCCCCATTTCAAAGTAGCGGGTTCTCAGCCACGTCCTCCTCCTTCTTCCTCCTCCTC 1947

Qy   439 TTCCACCGCAAAAGATAGCCCGCAACGTGTTTCTGTTCAAACTGGGTGG 485
               |||| | |||| || ||||| || ||| || || |||||||||
Db   1946 ATCCTCCTTCCTCGCCCCTGTTCACCCTGGCCCTCCTCCCGGTGGTTGG 1900

RESULT 13
; US-10-504-973-47
; Sequence 47, Application US/10504973
; Publication No. US20060121459A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; CHAWLA, Narinder K.;
; APPLICANT: YUE, Henry; RICHARDSON, Thomas W.;
; APPLICANT: MARQUIS, Joseph P.; GORVAD, Ann E.;
; APPLICANT: BECHA, Shanya D.; KABLE, Amy E.;
; APPLICANT: SWARNAKAR, Anita; JIN, Pei;
; APPLICANT: HAWKINS, Phillip R.; CHIEN, David;
; APPLICANT: RAMKUMAR, Jayalaxmi; LEHR-MASON, Patricia M.;
; APPLICANT: TRAN, Uyen K.; HAFALIA, April J.A.;
; APPLICANT: BAUGHN, Mariah R.; LEE, Soo Yeun;
; APPLICANT: JIAN, Xin; JACKSON, Alan A.;
; APPLICANT: KHARE, Reena; BULLOCH, Sean A.
; TITLE OF INVENTION: RECEPTORS AND MEMBRANE-ASSOCIATED PROTEINS
; FILE REFERENCE: PF-1381 PCT
; CURRENT APPLICATION NUMBER: US/10/504,973
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: US 60/358,279
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/364,338
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/375,657
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/376,669
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 60/379,837
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/379,853
; PRIOR FILING DATE: 2002-05-10
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PERL Program
;
; SEQ ID NO 47
; LENGTH: 2193
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7506852CB1
US-10-504-973-47

Query Match   3.7%; Score 48.2; DB 6; Length 2193;
Best Local Similarity   42.8%; Pred. No. 0.001;
Matches 242; Conservative   0; Mismatches 323; Indels   0; Gaps   0;

Qy   571 TATAAGAGGAATTGTCACCAGGCCCAAGGCCGTGGCTGTAGCCTTTTGCCTGATAGTGAGGACCATA 630
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Db   706 TACAAGATGGTGGTGACCCCCCGAGGGGGGCGGGGTGGGCCATAGCGCGGCTGCTGAGATCCTC 765

Qy   631 GCCATTGTGATCCGCGTGCTCCTGGGCTGGAACGCGGAGAAACTGCAAATCTGTT 690

RESULT 15
US-10-449-902-19898
; Sequence 19898, Application US/10449902

Query Match   3.6%;   Score 48;   DB 6;   Length 48;
Best Local Similarity   100.0%;   Pred. No. 0.00016;
Matches   48;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy 40 CGCACCATCACCACTGACCTCCTGGGAGAGTCCCTTCCAAGAGAGAAGATG 87
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Db  1 CGCACCATCACCACTGACCTCCTGGGAGAGTCCCTTCCAAGAGAGAAGATG 48
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RESULT 14
US-10-521-428A-6
; Sequence 6, Application US/10521428A
; Publication No. US20060115816A1
GENERAL INFORMATION:
; APPLICANT: Vu, Huy Khang
; APPLICANT: Groblewski, Thierry
; APPLICANT: Greasley, Peter
; TITLE OF INVENTION: Splice Variant Cannabinoid Receptor (CB1B)
; FILE REFERENCE: A5ZD-P01-750
; CURRENT APPLICATION NUMBER: US/10/521,428A
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 0202240-8
; PRIOR FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 48
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence of oligonucleotide used to delete polynucleotides
; OTHER INFORMATION: encoding human CB1b receptor N-terminus
US-10-521-428A-6

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Db  766 TCCTTCCGTTGGTGGGACTGAGACCCTATGTTGTTGGCTGGACAACAATCTGAGTGGCGGTGGGACGGG 825
Db  691 TGCTCAGAGACATTTTCCCACACATTGATGAAAACCTACCTTGATGTTCTTGGATTCGGGGTCACC 750
Db  826 GCCTGGGCAGCCAAACGGCCAGCATGGGGGGAGCCCGTGATCAAGTGCCGACTTCGAGAAGGTC 885
Db  751 AGGGTACTGCTTCGTTCATCGTGTATGCGTACATGTATATTCTCTGGAAGGCTCACAGC 810
Db  886 ATCAGCATGGGAGTACATGGTCTACTCAACTTCTTTGTGTGGTGCGTGCCCCGCTTCTC 945
Db  751 AGGGTACTGCTTCGTTCATCGTGTATGCGTACATGTATATTCTCTGGAAGGCTCACAGC 810
Qy  811 CACGCCGTTCGGCATGATTCAGCGTGGCGCACCCAGAAAGAGCATCATCATCCACACGGTCTGAG 870
Db  946 CTCATGGTTCCTCATCTACCTGGAGGGTCTTCTACCTAATCCGGAGAGGTCTCAACAAGAAG 1005
Qy  871 GATGGGAAGGTACAGGTGACCCGGCCCAGACCAAGCCCGCTAGGTATGGCAGTTCACCAAG 930
Db 1006 GTGTCGGCCTCCTCCGGCGGACCCGGACCAGGAGTACTATGGAGGAAGACATGCCAAG 1065
Qy  931 ACCTGGTCTCGATCCTGGGTGGTTGATCATCTGCTGGGGGCCCTGTGCTTGCAATCATG 990
Db 1066 TCGCTGGCCCCTATCATCCTCTTTCCCTCAGCTGGCTTGGTGCCGTGCCATCCTCAAC 1125
Qy  991 GTGTATGATGTCTTTGGGAAGATGAACACAAGCTCATTAAGACGGTGTTTGCATTCTGCAGT 1050
Db 1126 TGCATCACCCTTCTTCTGCCCGTCCTGCCACACACCCCAGCATCCTTAACACCTACATTGCCATC 1185
Qy 1051 ATGCTTCTTGCCTGTCTGACTCACCGTGAAACCCCATCAATCATGTGCTTCTGAGGAGTAAGGAC 1110
Db 1186 TTCCTCACGCACGGCAACTCGGGCCATGAACCCCATTGTCTATGCCTTCCGCAGTCCAGGAG 1245
Qy 1111 CTGGCGACACGCTTTCCGGAGCATGT 1135
Db 1246 TTCCGGGTCACCTTCTTCTTAAGATTT 1270
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; Publication No. US20060123505A1
GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 19898
; LENGTH: 1936
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK070238
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-19898

Query Match   3.5%;   Score 46.4;   DB 6;   Length 1936;
Best Local Similarity   49.2%;   Pred. No. 0.003;
Matches   122;   Conservative   0;   Mismatches   126;   Indels   0;   Gaps   0;

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Qy 297 GGAGAACCTCCTCGGTGTGCGTGCGGTCATCCTCACTCCCGGCAGCCTCCGGCAGGCCTTC 356
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Db 525 GGTGAATCCTCACCGCACCGCCATGAGGCGTCATCCTCCTCCCCATCTACCTCTTTGCCACCCGGAT 584
Qy 357 CTACCACTTCATGGGGCAGCCCTGCGCGGTGGCGACCTCCTGGGGGAGTGTGTCATTTTTGTCTA 416
        | |||||||||||||||| ||| | |||| |
Db 585 CCTCCGCTTCTTCCACCCAGGACGACGAGATGGCCGCGTTCCTCGCCACGCCGGTTCTCTCCCCTCTA 644
Qy 417 CAGCTTCATTGACTTCCACGTGTTCCACGCGAAAAGATAGCCGCAAACGTGTTGTTCTGGTTCAA 476
        |||||||| || ||||||| | |||
Db 645 CATGATCCCCAGCTCTTCGCCCTACGGCCCTCAAACTTCCCCATCCAGAAGTTCCTCCAGGC 704
Qy 477 ACTCGGGTGGGGTCACGGCGCTCCTTCACTCGCTCCGTGGGCAGCCTGTTGTTCCTCACAGCCAT 536
        | |||||||| |||||||||| |||| ||
Db 705 CCAGAGCAAGGTCATGGCCATGGCGCGGCCGTCTCGGCGGGCGGTGGTGCTGCTGTTCCACGTGCGG 764
Qy 537 CGACACAGGT 544
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Db 765 GCTCACGT 772
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Search completed: June 17, 2006, 00:21:26
Job time : 71 secs

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OM nucleic - nucleic search, using sw model

                        GenCore version 5.1.9
                        Copyright (c) 1993 - 2006 Bioacceleration Ltd.

Run on:         June 16, 2006, 23:47:50 ; Search time 1644 Seconds
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                                           9865.985 Million cell updates/sec

Title:          US-10-521-428A-1
Perfect score:  1320
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Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters:     37784340

Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

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                2: /EMC_Celera_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                3: /EMC_Celera_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                4: /EMC_Celera_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
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               14: /EMC_Celera_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
               15: /EMC_Celera_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
               16: /EMC_Celera_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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Result              %      Query
No.     Score   Match  Length  DB  ID                  Description
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 1     1259.4   95.4   5665    8   US-10-764-425-72      Sequence 72, Appl
 2     1259.4   95.4   5665    9   US-10-482-029-171     Sequence 171, App
 3     1259.4   95.4   5665   10   US-10-851-667A-10     Sequence 24, Appl
 4     1257.8   95.3   1419    7   US-10-029-386-24875   Sequence 24875, A
 5     1257.8   95.3   1755    6   US-10-225-567A-83     Sequence 83, Appl
 6     1257.8   95.3   1755    6   US-10-295-027-235     Sequence 235, Appl
 7     1257.8   95.3   1755   15   US-11-127-877-2       Sequence 2, Appli
 8     1257.8   95.3   5480   13   US-11-019-829-27      Sequence 27, Appl
 9     1257.8   95.3   5653    6   US-10-208-408-52      Sequence 52, Appl
10     1256.2   95.2   1419   10   US-10-521-420-2       Sequence 2, Appli
11     1256.2   95.2   1419   10   US-10-521-420-3       Sequence 3, Appli
12     1256.2   95.2   2135    7   US-10-101-510-715     Sequence 715, App
13     1256.2   95.2   2135    7   US-10-305-720-1450    Sequence 1450, Ap
14     1256.2   95.2   2135    8   US-10-641-643-1469    Sequence 1469, Ap
15     1256.2   95.2   5651    9   US-10-101-510-409     Sequence 409, App
16     1254.6   95.0   1419    3   US-09-826-509-468     Sequence 468, App
17     1254.6   95.0   1419    9   US-09-925-095-468     Sequence 468, App
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18     1254.6   95.0   1419   10   US-10-521-420-4       Sequence 4, Appli
19     1251.4   94.8   5472    3   US-10-295-027-237     Sequence 237, App
20     1209.8   91.7   1551    3   US-09-823-245A-513    Sequence 513, App
21     1151     87.2   1252    7   US-10-295-027-239     Sequence 239, App
22     1151     87.2   1252   13   US-11-019-829-28      Sequence 28, Appl
23     1049.2   79.5   5489   16   US-11-136-527-2129    Sequence 2129, Ap
24     795.8    60.3    993   16   US-11-128-061-837     Sequence 837, App
25     795.8    60.3    993   16   US-11-128-049-4479    Sequence 4479, Ap
26     506.2    38.3    600   16   US-11-060-756-6492    Sequence 6492, Ap
27     506.2    38.3    600   16   US-11-060-756-6491    Sequence 6491, Ap
28     498.4    37.8    500    7   US-10-521-386-11154   Sequence 11154, A
29     412      31.2    600   13   US-11-060-756-2219    Sequence 2219, Ap
30     412      31.2    600   13   US-11-060-756-2220    Sequence 2220, Ap
31     412      31.2    600   16   US-11-330-773-928     Sequence 928, App
32     412      31.2    600   13   US-11-330-773-929     Sequence 929, App
33     252.4    19.1   3715   11   US-10-330-773-928     Sequence 928, App
34     252.4    19.1  44617   11   US-10-330-773-929     Sequence 929, App
35     246.8    18.7  21906   11   US-11-128-049-4479    Sequence 931, App
36     246.8    18.7   1906   11   US-10-330-773-931     Sequence 931, App
37     246.8    18.7   1776   10   US-10-851-667A-25     Sequence 25, Appl
38     245.2    18.6   1083    7   US-10-290-078-2       Sequence 2, Appli
39     245.2    18.6   1776    6   US-10-225-567A-85     Sequence 85, Appl
40     245.2    18.6   1790    7   US-10-290-078-1       Sequence 1, Appli
41     245.2    18.6   1790    8   US-10-305-720-1359    Sequence 1359, Ap
42     245.2    18.6   1790    8   US-10-641-643-1398    Sequence 1398, Ap
43     242.8    18.4   2926   16   US-11-136-527-3556    Sequence 3556, Ap
44     240.4    18.2   1083    9   US-09-826-509-470     Sequence 470, App
45     240.4    18.2   1083    9   US-10-925-095-470     Sequence 470, App
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ALIGNMENTS

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RESULT 1
US-10-764-425-72
Sequence 72, Application US/10764425
; Publication No. US20040146921A1
; GENERAL INFORMATION:
;  APPLICANT: Bayer Pharmaceuticals Corporation
;  APPLICANT: Eveleigh, Deepa
;  APPLICANT: Bigwood, Douglas
;  APPLICANT: Taylor, Ian
;  TITLE OF INVENTION: EXPRESSION PROFILES FOR COLON CANCER AND METHODS OF USE
;  FILE REFERENCE: 5151
;  CURRENT APPLICATION NUMBER: US/10/764,425
;  CURRENT FILING DATE: 2004-01-23
;  PRIOR APPLICATION NUMBER: 60/442,582
;  PRIOR FILING DATE: 2003-01-24
;  NUMBER OF SEQ ID NOS: 191
;  SOFTWARE: Patentin version 3.2
; SEQ ID NO 72
;  LENGTH: 5665
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-764-425-72

  Query Match             95.4%;  Score 1259.4;  DB 8;  Length 5665;
  Best Local Similarity   99.5%;
  Matches 1263;  Conservative   0;  Mismatches   6;  Indels   0;  Gaps   0;

Qy         52 ACTGACCTCCTGTGGGAAGTTCCCTTCCAAGAAGAAGATGACTGGGGGAGAACAACCCCCAGCTA 111
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Db        272 ACTTCCTTTAGGGGAAGTCCCTTCCAAGAAGAAGATGACTGCGGGAGACAACCCCCAGCTA 331

Qy        112 GTCCCAGCAGGACCAGGTGAACATTACAGAATTTTACACAACAAGTCTCTCTGGTCCTTCAAG 171
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Db        332 GTCCCAGCAGGACCAGGTGAACATTACAGAATTTTACACAACAAGTCTCTCTGGTCCTTCAAG 391

Qy        172 GAGAATGAGGAGGAGAACATCCAGTGTGGGGAGAGACTTCATGGAACATTAGAGTGTTTCATGGTC 231
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Db        392 GAGAATAGAGGAGAACATCCAGTGTGGGGAGAGACTTCATGGACATTAGAGTGTTTCATGGTC 451

Db        232 CTGAACCCCAGCCAGCGACCAGCTGGCCATTGCAGTGTCCTGTGTCCCTCAGCGCTGGCGGCCACTTCACG 291
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Db   1532 GCTCTGTGA 1540
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RESULT 2
US-10-482-029-171
; Sequence 171, Application No. US/10482029
; Publication No. US2005003744SA1
; GENERAL INFORMATION:
; APPLICANT: ODIN medical A/S
; TITLE OF INVENTION: Oncology drug innovation
; FILE REFERENCE: P 573 PC00
; CURRENT APPLICATION NUMBER: US/10/482,029
; CURRENT FILING DATE: 2003-12-29
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 171
; LENGTH: 5665
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-482-029-171

Query Match   95.4%;   Score 1259.4;   DB 9;   Length 5665;
Best Local Similarity   99.5%;   Pred. No. 0;   Mismatches 6;   Indels 0;   Gaps 0;
Matches 1263;   Conservative   0;   Mismatches 6;   Indels 0;   Gaps 0;
```

The remainder of the page consists of a two‑sequence (Qy / Db) nucleotide alignment printed in successive blocks, each showing a query line (Qy), a match line (||||…), and a database line (Db) with flanking residue‑position numbers (e.g. Qy 52 … 111; Db 272 … 331; continuing in increments of 60 through Qy 1312 … 1320 and Db 1532 GCTCTGTGA 1540).

RESULT 3
US-10-851-667A-24
Sequence 24, Application US/10851667A
Publication No. US20050260608A1
GENERAL INFORMATION:
APPLICANT: Zimmer, Andreas
APPLICANT: Karsak, Meliha
APPLICANT: de Vernejoul, Marie-Christine
APPLICANT: Bab, Ital
APPLICANT: Shohami, Esther
APPLICANT: Mechoulam, Raphael
TITLE OF INVENTION: METHODS, KITS AND PHARMACEUTICAL COMPOSITIONS FOR DIAGNOSING,
TITLE OF INVENTION: DELAYING ONSET OF, PREVENTING AND/OR TREATING OSTEOPOROSIS
FILE REFERENCE: 28030
CURRENT APPLICATION NUMBER: US/10/851,667A
CURRENT FILING DATE: 2004-05-24
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.2
SEQ ID NO 24
LENGTH: 5665
TYPE: DNA
ORGANISM: Homo sapiens
US-10-851-667A-24

Query Match   95.4%;   Score 1259.4;   DB 10;   Length 5665;
Best Local Similarity   99.5%;   Pred. No. 0;
Matches 1263;   Conservative 0;   Mismatches 6;   Indels 0;   Gaps 0;

```
Qy   52 ACTGAACCTCTGGGAAGTTCCCTTCCAAGAGAGAAGATGAGTACTCGGGACAACAACCCCAGCTA 111
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  272 ACTTCCTTTAGGGAAGTTCCCTTCCAAGAGAGAAGATGACTCGGGAGACAACCCCAGCTA 331
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Qy  112 GTCCCCAGCGAGACCAGGGTGAACATTACAGAGAATTTTACAGACAAGTCTCTCGTCCTTCAAG 171
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  332 GTCCCGACGAGACCAGGGTGAACATTACAGAGAATTTTACAGACAAGTCTCTCGTCCTTCAAG 391
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Qy  172 GAGAATGAGGGAGGAACATCCAGTGTGGGGGAGAACTTCATGGAACATAGAGTGTTTCATGGTC 231
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  392 GAGAATGAGGGAGGAACATCCAGTGTGGGGGAGAACTTCATGGAACATAGAGTGTTTCATGGTC 451
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Qy  232 CTGAACCCCAGCCAGCAGTCCATTGCAGTCCTTCAGGTCCTCAGCCTGGCCACCCTTCACG 291
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  452 CTGAACCCCAGCCAGCAGTCCATTGCAGTCCTTCAGGTCCTCAGCCTGGCCACCCTTCACG 511
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Qy  292 GTCCTGGAGAACCTTCGTCGTGGCCTCATCCTCCACTCCACCTCCCCGGCAGCCTCCGGCAGG 351
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  512 GTCCTGGAGAACCTTCCTGGTTGGCCTCATCCTCCACTCCACCTCCCCGGCAGCCTCCGGCAGG 571
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Qy  352 CCTTCCTACCCACTTCATCTGGGCAGCCTGGCCTATAGGATGCAGCCTATAGGATGCAGG 411
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  572 CCTTCCTACCCACTTCATCTGGGCAGCCTGGCCTATAGGATGCAGCCTATAGGATGCAGG 631
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Qy  412 GTCTACAGCTTCATTGACTTCCACGTGTTCCACGCAAAGATAGCCGCAAGGTGTTTCTG 471
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  632 GTCTACAGCTTCATTGACTTCCACGTGTTCCACGCAAAGATAGCCGCAAGGTGTTTCTG 691
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Qy  472 TTCAAACTGGGTGGGGTCACGGCCCTCCACTGCCTCCGTGGGCGAGGCCTGTTCCTCACA 531
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  692 TTCAAACTGGGGTGGGGTCACGGCCCTCCACTGCCTCCGTGGGCGAGGCCTGTTCCTCACA 751
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```
Qy  532 GCCATCGACAGGTACATATCCATTCACACAGGCCCCTATAGAGGATTGTCACCAGG 591
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  752 GCCATCGACAGGTACATATCCATTCACACAGGCCCCTATAGAGGATTGTCACCAGG 811
```

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Qy  592 CCCAAGGCCGTGGTAGCGTTTTGCCTGATGGACCATAGCCATTGTGATCGGCGTGCTG 651
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  812 CCCAAGGCCGTGGTAGCGTTTTGCCTGATGTGGACCATAGCCATTGTGATCGGCGTGCTG 871
```

```
Qy  652 CCTTCTCCTGGGGCTGGAACTGCGAGAAACTGCAATCTGTTTTGCTCAGACATTTCCCACAC 711
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  872 CCTTCTCCTGGGGCTGGAACTGCGAGAAACTGCAATCTGTTTTGCTCAGACATTTCCCACAC 931
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Qy  712 ATTGATGAAACCTACCTGAGTTCTGGAATCGCGGGGGTCACCGGCTACTCCTTCTGTTCATC 771
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  932 ATTGATGAAAACCTACCTGAGTTCTGGAATCGCGGGGGTCACCGGCTACTCCTTCTGTTCATC 991
```

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Qy  772 GTGTATCGTACATGTATATTCTCTGGAAGGCTCACAGCCAGCCGTGTCCGCATGATTCAG 831
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  992 GTGTATCGGTACATGTATATTCTCTGGAAGGCTCACAGCCAGCCGTGTCCGCATGATTCAG 1051
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```
Qy  832 CGTGGCACCCAGAAGAGCATCATCATCCACACGCTCTGAGGATGGGGAAGGTACAGGTGACC 891
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1052 CGTGGCACCCAGAAGAGCATCATCATCCACACGCTCTGAGGATGGGGAAGGTACAGGTGACC 1111
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Qy  892 CGGCCAGACCAAGCCCCGGCCATGGACATTAGGTTAGCCAAGAACCCTGGGTCCTGATCCTGGTG 951
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1112 CGGCCAGACCAAGCCCCGGCCATGGACATTAGGTTAGCCAAGAACCCTGGGTCCTGATCCTGGTG 1171
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Qy  952 GTGTTGATCATCTGCTGGGGGCCCTCTCCTTGCTTTGTTTTGCTTGGGGGGCCCTCACG 1011
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1172 GTGTTGATCATCTGCTGGGGGCCCTCTCGCTTGCTTTTGTTTTGCTTGGGGGGCCCTCACG 1231
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Qy 1012 ATGAACAAGCTCATTAAGACAGGTGTTTGCATTCTGCAGTATGGTTTGCCTGTTGGGTGAACTCC 1071
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1232 ATGAACAAGCTCATTAAGACAGGTGTTTGCATTCTGCAGTATGGTTTGCCTGTTGGGTGAACTCC 1291
```

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Qy 1072 ACCGTGAACCCCATCATCATCTATCGCTTCGGACACGCCTTCCGGAGC 1131
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db 1292 ACCGTGAACCCCATCATCATCTATCGCTTCGGACACGCCTTCCGGAGC 1351
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Qy 1132 ATGTTTCCCTCTTGTGAAGGCACTGCGCAGCCTCTGGATAACAGCAACGCGACTCGGAC 1191
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1352 ATGTTTCCCTCTTGTGAAGGCACTGCGCAGCCTCTGGATAACAGCAACGCGACTCGGAC 1411
```

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Qy 1192 TGCCTGCACAAACACGCAAACAAATGCAGCCAGTGTTCACAGGGCGCGGAAAGCTGCATC 1251
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1412 TGCCTGCACAAACACGCAAACAAATGCAGCCAGTGTTCACAGGGCGCGGAAAGCTGCATC 1471
```

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Qy 1252 AAGAGCACGGTCAAGATTGCCAAGGTAACCAGTGTCTGTGTTCACAGACACGTCTGCCGAG 1311
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1472 AAGAGCACGGTCAAGATTGCCAAGGTAACCAGTGTCTGTGTCCACAGACACGTCTGCCGAG 1531
```

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Qy 1312 GCTCTCGTGA 1320
           ||||||||||
Db 1532 GCTCTCGTGA 1540
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Db　1412　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　1412　TGGCTTGCACAAACACGCAAAAACAATGCAGCCAGTGTTCACAGGGCCGGCCGAGAAAGCTGCATC　1471
Db　1472　AAGAGCACGGTCAAGATTGCCAAGGTAACCAAGTCTGTGTCCACAGACACGTCTGCCGAG　1531
Qy　1252　AAGAGCACGGTCAAGATTGCCAAGGTAACCAAGTGTTCACAGGGCCGGCCGAGAAAGCTGCATC　1311
Qy　1472　AAGAGCACGGTCAAGATTGCCAAGGTAACCAAGTCTGTGTCCACAGACACGTCTGCCGAG　1531
Qy　1312　GCTCTGTGA　1320
Db　1532　GCTCTGTGA　1540

RESULT 4
US-10-029-386-24875
Sequence 24875, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: ABOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10,029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 24875
; LENGTH: 1419
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL136096.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.22
; OTHER INFORMATION: SWISSPROT HIT: P21554, EVALUE 0.00e+00
; OTHER INFORMATION: NT HIT: gi16173524, EVALUE 0.00e+00
; OTHER INFORMATION: EST_HUMAN HIT: M77952.1, EVALUE 0.00e+00
US-10-029-386-24875

Query Match　95.3%;　Score 1257.8;　DB 7;　Length 1419;
Best Local Similarity　99.4%;　Pred. No. 0;
Matches 1262;　Conservative　0;　Mismatches　7;　Indels　0;　Gaps　0;

Qy　52　ACTGACCTCCTGGGAGAGTCCCTTCCAAGAGAAGAGAAGGAGAGAAGAGTACTGGGGAGCAACAACCCCAGCTA　111
Db　52　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　112　GTCCCAGCAGACCAGGTGAACATTACAGAATTTTACAGAAGAGGATGACTGCGGGAGCAACAACCCCAGCTA　171
Db　112　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　151　ACTTCCTTTAGGGAGAGTCCCTTCCAAGAGAAGAGAAGGAGAGAAGAGTACTGGGGAGCAACAACCCCAGCTA　210
Db　151　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　211　GTCCCAGCAGACCAGGTGAACATTACAGAATTTTACAGAAGAGTCTCTTCGTCCTTCAAG　270
Db　211　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　172　GAGAATGAGGAGGAAACATTCCAGTGTGTGGGGAGAACTTCATGGACATAGAGTGTTTCATGGTC　231
Db　172　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　271　GAGAATGAGGAGGAAACATTCCAGTGTGTGGGGAGAACTTCATGGACATAGAGTGTTTCATGGTC　330
Db　271　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　232　CTGAACCCCAGCCAGCAGCTGGCCATTGCGAGTCCAGTCCAGTCCACGTCCCTGCAGG　291
Db　232　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　331　CTGAACCCCAGCCAGCAGCTGGCCATTGCAGTCCAGTCCAGTCCACGTGCCACCTTCACG　390
Db　331　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　292　GTCCTGAGAACCTCCTGCTGCTGTGGCGTCATCTCCACTCACTCCCGCTCCGCTGCAGG　351
Db　292　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　391　GTCCTGAGAACCTCCTGGTGCTGTGGCGTCATCCTCCACTCCGCCCGCAGCGCTGCAGG　450
Db　391　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　352　CCTTCCTTACCACTTCATCGGAGCAGCCTCGGCGCGTGGCGCGACACTTCCTCTGGGGAGTGTGTCATTTTT　411
Db　352　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　451　CCTTCCTTACCACTTCATCGGAGCAGCCTCGGCGCGTGGCGCGACACTTCCTCTGGGGAGTGTGTCATTTTT　510
Db　451　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　412　GTCTACAGCTTCATTGACTTCCACGTGTTCCACGGCAAAGATAGCCGCGAAACGTGTTTCTG　471
Db　412　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　511　GTCTACAGCTTCATTGACTTCCACGTGTTCCACGGCAAAGATAGCCGCGAAACGTGTTTCTG　570
Db　511　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　472　TTCAAACTGGGGTGGGGGTCACGGCCTCCTTCACTGCCTGGCAGCCGCTGTTCCTCACA　531
Db　472　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db　571　TTCAAACTGGGGTGGGGGTCACGGCCTCCTTCACTGCCTGGCAGCCGCTGTTCCTCACA　630
Qy　532　GCCATCGACAGGTACAGTATATCCATTCACAGGGCCCCCTGGCCTATAAGAGAGGATTGCCACCAGG　591
Db　532　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　631　GCCATCGACAGGTACAGTATATCCATTCACAGAGGCCCCTGGCCTATAAGAGAGGATTGCCACCAGG　690
Db　631　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　592　CCCAAAGGCCGTGGTGTGAGCGTTTTGCCCTGATGTGGACACATAGCCATTGTGATCGCGTG　651
Db　592　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　691　CCCAAAGGCCGTGGTGTGGGCGTTTTGCCCTGATGTGGACACATAGCCATTGTGATCGGCTG　750
Db　691　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　652　CCTCTCCTGGGCTGGGAACTGCGAGAAACTGCAATCTGTTTGCTCAGAGCATTTTCCCACAC　711
Db　652　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　751　CCTCTCCTGGGCTGGGAACTGCGAGAAACTGCAATCTGTTTGCTCAGAGCATTTTCCCACAC　810
Db　751　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　712　ATTGATGAAAACCTTACCTGATGTGTTCTGGATCGGTGGGGTCACCAGCCGGTACTGCTTCTCATC　771
Db　712　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　811　ATTGATGAAAACCTTACCTGATGTGTTCTGGATCGGTGGGGTCACCAGCCGGTACTGCTTCTCATC　870
Db　811　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　772　GTGTATGTGCGTACATGTATATTCTCTGGAAAGGCTCACAGCCACCGGCCAGCGGTACTGCAGGATGATCAG　831
Db　772　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　871　GTGTATGTGCGTACATGTATATTCTCTGGAAGGCTCACAGCCACCGGTCCGCATGATCAG　930
Db　871　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　832　CGTGGGCACCCAGAAGAGGCATCATCATCCACACAGTCTGAGGATGGGAGGTACAGGTGACC　891
Db　832　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　931　CGTGGGCACCCAGAAGAGGCATCATCATCCACACGTCTGAGGATGGGAGGTACAGGTGACC　990
Db　931　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　892　CGGCCAGACCAAGCCCGGACATTAGGGTTAGCCAAGACCCTGGTCCTTGATCCTGGTG　951
Db　892　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　991　CGGCCAGACCAAGCCCGGATGGACATTAGGGTTAGCCAAGACCCTGGTCCTTGATCCTGGTG　1050
Db　991　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　952　GTGTTGATCATCCTGCTGGGGCCCCTTCCTCCTTGTTTGCAAATCATGGGTGTATGATGTCTTGGGAAG　1011
Db　952　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　1051　GTGTTGATCATCCTGCTGGGGCCCCTTCTCCTTGTTTGCAAATCATGGGTGTATGATGTCTTTGGGAAG　1110
Db　1051　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　1012　ATGAACAAAGCTCATTAAGACGCGTGTTTGCATTCTGCAGTAGTGCTTCTGCTTGCTGCTGCGAACTCC　1071
Db　1012　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　1111　ATGAACAAAGCTCATTAAGACGCGTGTTTGCATTCTGCAGTAGTGCTTCTGCTTGCTGCTGCGAACTCC　1170
Db　1111　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　1072　ACCGTGAACCCCATCATCTATGCTTCTGAGGAGTAAGGACTGAAGCTGGAAGTAAGGCTTCCGGAGC　1131
Db　1072　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　1171　ACCGTGAACCCCATCATCTATGCTTCTGAGGAGTAAGGACTGAAGCTGGAAGTAAGGCTTCCGGAGC　1230
Db　1171　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　1132　ATGTTTCCCTCTTGTGAAGGCACTGCGGCAGCCTCTGGATAACAGCATGGGGGGGGGACTCGGAC　1191
Db　1132　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　1231　ATGTTTCCCTCTTGTGAAGGCACTGCGGCAGCCTCTGGATAACAGCATGGGGGGGGGACTCGGAC　1290
Db　1231　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　1192　TGGCCTGCACAAACACGCAAAACAATGCAGCCAGTGTTCACAGGGCCGGCGAAAGCTGCATC　1251
Db　1192　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　1291　TGGCCTGCACAAACACGCAAAACAATGCAGCCAGTGTTCACAGGGCCGGCGAAAGCTGCATC　1350
Db　1291　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　1252　AAGAGCACGGTCAAGATTGCCAAGGTAACCAAGTCTGTGTCCACAGACACGTCTGCCGAG　1311
Db　1252　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　1351　AAGAGCACGGTCAAGATTGCCAAGGTAACCAATGTCTGTCGTCCACAGACACGTCTGCCGAG　1410
Db　1351　|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy　1312　GCTCTGTGA　1320
Db　1312　|||||||||
Db　1411　GCTCTGTGA　1419

RESULT 5
US-10-225-567A-83
Sequence 83, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144

```
;
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
;
; SEQ ID NO 83
; LENGTH: 1755
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-83

Query Match    95.3%;  Score 1257.8;  DB 6;  Length 1755;
Best Local Similarity   99.4%;  Pred. No. 0;
Matches 1262;  Conservative  0;  Mismatches  7;  Indels  0;  Gaps  0;
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Qy       52 ACTGACCTTCTACCACTTCATCGGGCAGCGTCCCTTCCAAGAGAAGAAGATGACTGGGGAGGAGGACAACCCCAGCTA 111
Db      299 ACTTCCTTTAGGGGAAGTCCCTTCCAAGAGAAGAAGATGACTGGGGAGGAGGACAACCCCCAGCTA 358

Qy      112 GTCCCAGCAGACCAGGTGAACATTACAGAATTTTACACAGAAGTCTCTCTTCGTCCTTCAAG 171
Db      359 GTCCCAGCAGACCAGGTGAACATTACAGAATTTTACACAGAAGTCTCTCTTCGTCCTTCAAG 418

Qy      172 GAGAATGAGGAGGAGAACATCCAGTGTGGGGAGGAACTTCATGGACATAGAGTGTTTCATGTCTC 231
Db      419 GAGAATGAGGAGGAGAACATCCAGTGTGGGGAGGAACTTCATGGACATAGAGTGTTTCATGTC 478

Qy      232 CTGAACCCCAGCCAGCAGCAGCTGGGCCATTGGCAGTCCGTGCACTTCACG 291
Db      479 CTGAACCCCAGCCAGCAGCAGCTGGGCCATTGGCAGTCCGTGCACTTCACG 538

Qy      292 GTCCTGGAGAACTTCTCCTGGTGTGCTGCGTCATCCTCCACTCCCGCAGG 351
Db      539 GTCCTGGAGAACTTCTCGGTGTGCGTCATCCTCCACTCCCGCAGG 598

Qy      352 CCTTCCTACCACTTCATCGGGCAGCGCCTGCCCTGCGGTGGCAGACCTTCTTCTGGGAGTGTGCATTTTT 411
Db      599 CCTTCCTACCACTTCATCGGGCAGCGCCTGCCCTGCGGTGGCAGACCTTCTTCTGGGAGTGTGCATTTTT 658

Qy      412 GTCTACAGCTTCATTGACTTCCACGTGTTCCACCGGCCAAAGAGTAGCCGGCAAGCGTGTTCTG 471
Db      659 GTCTACAGCTTCATTGACTTCCACGTGTTCCACCGGCCAAAGAGTAGCCGGCAAGCGTGTTCTG 718

Qy      472 TTCAAACTGGGTGGGGTGGGGTCACGGGCCCTCCTTCACTGCCTCCTGCTGTTCCTCACA 531
Db      719 TTCAAACTGGGGTGGGGGTCACGGGCCCTCCTTCACTGCCTCCTCCGTGTTCCTCACA 778

Qy      532 GCCATCGACACAGGTACATATCCAATTCACAGCCCCCTGGCCTATAAGCAGGATTGTTCACCAGG 591
Db      779 GCCATCGACACAGGTACATATCCAATTCACAGCCCCCTGGCCTATAAGCAGGATTGTTCACCAGG 838

Qy      592 CCCAAGGCCGTGGTAGGCGTTTTGCCTGATGTGGACCAATAGCCATTGTTGATCGCCGTGGCTG 651
Db      839 CCCAAGGCCGTGGTGGGCGTTTTGCCTGATGTGGACCAATAGCCATTGTTGATCGCCGTGGCTG 898

Qy      652 CCTCTCCTGGGGCTGGGAAACTGCGAATCTGTTGTTGCTCAGACATTTCCCACAC 711
Db      899 CCTCTCCTGGGGCTGGGAACTGCGAATCTGTTTGCTCAGACATTTTCCCACAC 958

Qy      712 ATTGATGAAAACCTTACTTCGATGTTCTCTGATCGGGGTCACCGGGTACTGCTTCTGTTCATC 771
Db      959 ATTGATGAAACCTTACCTGATGTTCTCTGATCGGGGTCACCGGGTACTGCTTCTGTTCATC 1018

Qy      772 GTGTAATCGGTACATGTATATTCTCTGGAAGGGCTTACAGCGCCACGCTCCGCATGACATTCAG 831
Db     1019 GTGTAATCGGTACATGTATATTCTCTGAAGGGCTTACAGCGCCACGCTCCGCATGACATTCAG 1078

Qy      832 CGTGGCACCCAGAGAGAGCATCATCATCCAACGTCTCGAGGGATGGGAAGGTACAGGTGACC 891
Db     1079 CGTGGCACCCAGAGAAGAGGCATCATCATCCAACGTCTCGAGGGATGGGAAGGTACAGGTGACC 1138

Qy      892 CGGCCAGACCAAGCCCCGCCCCATGGACAATTAGGTTGTAGCCAAGACCCTGGTTCCTGATTCCTCGGTG 951
Db     1139 CGGCCAGACCAAGCCCCGCCCCATGGACAATTAGGTTGTAGCCAAGACCCTGGTTCCTGATTCCTCGGTG 1198

Qy      952 GTGTTGATCATCTGCTGGGGCCCTTCCTGCTTGCTTGCAATCATGGTGATGTCTTTGGGAAG 1011
Db     1199 GTGTTGATCATCTGCTGGGGCCCTTCCTGCTTGCTTGCAATCATGGTGATGTCTTTGGGAAG 1258

Qy     1012 ATGAACAAGTCAATTAAGACGGGTGTTTGCATTCTGCAGTATGTGCTTGCTGCTGAACTCC 1071
Db     1259 ATGAACAAGTCATTAAGACGGGTGTTTGCATTCTGCAGTATGTGCTTGCTGCTGAACTCC 1318

Qy     1072 ACCGTGAACCCCATCATCTATGCTCTGGAGGAGTAAGGACTGCAGCAGCACGCTTTCCGGAGC 1131
Db     1319 ACCGTGAACCCCATCATCTATGCTCTGGAGGAGTAAGGACTGCAGCAGCACGCTTTCCGGAGC 1378

Qy     1132 ATGTTTCCCTCTTGTGAAGGCACTGCGCGAGCCTCTGGATAACAGCAGTGGGGGGGGACTGGGAC 1191
Db     1379 ATGTTTCCCTCTTGTGAAGGCACTGCGCGAGCCTCTGGATAACAGCAGTGGGGGGGGACTGGGAC 1438

Qy     1192 TGCCTGCACAAACACGCAAACAATGCAGCGCAGTGGTTCACAGAGGGGGGCAGAAAAGTGCATC 1251
Db     1439 TGCCTGCACAAACACGCAAACAATGCAGCGCAGTGGTTCACAGAGGGGGGCAGAAAAGTGCATC 1498

Qy     1252 AAGAGCACGGTCAAGATTTCCCAAGGTAACCATGTCTCGTGTTGTTCCACAGACACACGTCTGCCCAG 1311
Db     1499 AAGAGCACGGTCAAGATTTCCCAAGGTAACCATGTCTCGTGTTGTTCCACAGACACACGTCTGCCCAG 1558

Qy     1312 GCTCTGTGA 1320
Db     1559 GCTCTGTGA 1567
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RESULT 6
US-10-295-027-235
; Sequence 235, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynne, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-0125000US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 235
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;        LENGTH: 1755
;        TYPE: DNA
;        ORGANISM: Homo sapiens
US-10-295-027-235

Query Match      95.3%;   Score 1257.8;   DB 7;   Length 1755;
Best Local Similarity   99.4%;   Pred. No. 0;
Matches 1262;   Conservative   0;   Mismatches   7;   Indels   0;   Gaps   0;

Qy    52 ACTGACCTCCTGGGAGTCCCTTCCTTCCAAGAGAGAAGAAGATGATGACTGCGGGAGGACAACCCCCAGCTA 111
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Db   299 ACTTCCTTTAGGGAAGTCCCTTCCAAGAGAAGAAGATGACTGCGGGGAGACAACCCCAGCTA 358

Qy   112 GTCCCAGCAGGACCAGGTGAACATTACAGAAATTTACAACAAGTCTCTTCTCGTCCTTCAAG 171
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   359 GTCCCAGCAGGACCAGGTGAACATTACAGAAATTTACAACAAGTCTCTTCTCGTCCTTCAAG 418

Qy   172 GAGAATGAGGAGAGAACATCCAGTGTGGGGAGGAACTTCAGTGGACAATAGAGTGTTTCATGGTC 231
         |||||||||||| ||||||||||||||||||||||||||| |||||||||||||||||||||||
Db   419 GAGAATGAGGAGGAACATCCAGTGTGGGGAGGAACTTCAGTGGACAATAGAGTGTTTCATGGTC 478

Qy   232 CTGAACCCCAGCCAGCAGCTGGCCATTGCAGTCCTGTCCCTCACGCGTGGGCGCACCTTCACG 291
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   479 CTGAACCCCAGCCAGCAGCTGGCCATTGCAGTCCTGTCCCTCACGCGTGGGCGCACCTTCACG 538

Qy   292 GTCCTCGGAGAACCTCCTCGGGTGCTGTGGGTGGGTCANCCTCACTCACTCCCGCGCCTCCGCGCTGCAGG 351
         ||||| |||||||||||||||||||||||||     ||||||||||||||||||||||||||||||||||
Db   539 GTCCTCGAGAACCTCCTCGGGTGCTGTGGGTCANCCTCACTCACTCCCGCGCCTCCGCGCTGCAGG 598

Qy   352 CCTTCCTACCACTTCATCGGCAGCCTGGCGGTGGCAACCTCCTGGGAGGAGTGTCATTTTT 411
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   599 CCTTCCTACCACTTCATCGGCAGCCTGGCGGTGGCAACCTCCTGGGAGGAGTGTCATTTTT 658

Qy   412 GTCTACAGCTTCATTGACTTCACGGTGTTCACCGACAAAGATAGCACCTGTTGTTTCTG 471
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   659 GTCTACAGCTTCATTGACTTCACGGTGTTCACCGCAAAGATAGCCCGCAACCGTGTTTCTG 718

Qy   472 TTCAAACTGGGGTGGGGTCACGGCCCTCCTTCACTGCCTTCCTGGGCGGCAGCCGGTGTTCCTCACA 531
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   719 TTCAAACTGGGGTGGGGTCACGGCCCTCCTTCACTGCCTCCCGTGGGCAGCCGGAGGTGTTCCTCACA 778

Qy   532 GCCATCGACAGGTACATATTCATTCACAGGCCCCGGGCCTATAAGAGGAATTGTTGCCAGG 591
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   779 GCCATCGACAGGTACATATTCATTCACAGGCCCCGGGCCTATAAGAGGAATTGTTGCCAGG 838

Qy   592 CCCAAGCGCCGTGGTAGGCGTTTTGCCTGATGTGTGGACCATAGCCAATTGTGTGATCCCGTGCTG 651
         ||||||||||||||||      ||||||||||||||||||||||||||||||||||||||||||||
Db   839 CCCAAGCGCCGTGGTTTTGCCTGATGTGTGGACCATAGCCAATTGTGTGATCCCGTGCTG 898

Qy   652 CCTCTCCTGGGCGTGGGAGAACTGCAAATCTCGTTTGCTTGCTCAGACATTTTCCCACAC 711
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   899 CCTCTCCTGGGCGTGGGAGAACTGCAAATCTCGTTTGCTTGCTCAGACATTTTCCCACAC 958

Qy   712 ATTGATGAAACCTACCTGAGTTCTGGAATCGGGCGGGGTCACCAGGGCTACTTCTGTTCATC 771
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   959 ATTGATGAAACCTACCTGAGTTCTGGAATCGGGCGGGGTCACCAGGGTACTTCTGTTCATC 1018

Qy   772 GTGTATCGGTACATGTATATTCTCTGGAGAGGCTTCAGCGAACGCCGTCCGCATGAATTCAG 831
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1019 GTGTATCGGTACATGTATATTCTCTGGAGAGGCTTCAGCGAACGCCGTCCGCATGAATTCAG 1078

Qy   832 CGTGGGCACCCAGAAGAGAGCATCATCATCCACAGTCTTGAGGATGGGGAGGTACAGGGTGACC 891
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1079 CGTGGGCACCCAGAAGAGAGCATCATCATCCACAGTCTTGAGGATGGGGAGGTACAGGGTGACC 1138

Qy   892 CGGCCAGACCAAGCCCCGCCATGGACAGTTAGGTTAGCCAAGACCCGGTCGTCCTGGTG 951
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Db  1139 CGGCCAGACCAAGCCCCGCCATGGACATTAGGTTAGCCAAGACCCGGTCGTCCTGGTG 1198

Qy   952 GTGTTGATCATCTGCTGCTTCTCCTTGCGAATCATCATTGTATGATGTGTGTGTCTTTGGGAAG 1011
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1199 GTGTTGATCATCTGCTGCTTCTCCTTGCGAATCATCATTGTATGATGTGTGTGTCTTTGGGAAG 1258

Qy  1012 ATGAACAAGCTCATTAAGACGGTGTTGTTTGCATTCTGCAGTATGCTTCTGCCTGTCTGGAACTCC 1071
         |||||||||||||||||||||||||| ||||||||||||||||| |||||||||||| |||||||
Db  1259 ATGAACAAGCTCATTAAGACGGTGTTTGCAGTGTTTGCAGTATCTGCCTGCTGTCCTCC 1318

Qy  1312 GCTCTGTGA 1320
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Db  1559 GCTCTGTGA 1567
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RESULT 7
US-11-127-877-2

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;  Sequence 2, Application US/11127877
;  Publication No. US20050287565A1
;  GENERAL INFORMATION:
;    APPLICANT: Merchiers, Pascal G.
;    APPLICANT: Hoffmann, Marcel
;    APPLICANT: Spittaels, Koenraad F. F.
;    APPLICANT: Laenen, Wendy
;    TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
;    TITLE OF INVENTION: Amyloid-Beta Protein Production
;    FILE REFERENCE: P27,800-B USA
;    CURRENT APPLICATION NUMBER: US/11/127,877
;    CURRENT FILING DATE: 2005-05-12
;    PRIOR APPLICATION NUMBER: 60/570,352
;    PRIOR FILING DATE: 2004-05-12
;    PRIOR APPLICATION NUMBER: 60/603,948
;    PRIOR FILING DATE: 2004-08-24
;    NUMBER OF SEQ ID NOS: 590
;    SOFTWARE: Patentin version 3.3
;
;  SEQ ID NO 2
;    LENGTH: 1755
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-11-127-877-2

Query Match      95.3%;   Score 1257.8;   DB 15;   Length 1755;
Best Local Similarity   99.4%;   Pred. No. 0;
Matches 1262;   Conservative   0;   Mismatches   7;   Indels   0;   Gaps   0;

Qy    52 ACTGACCTCCTGGGAGTCCCTTCCTTCCAAGAGAGAAGAAGATGATGACTGCGGGAGGACAACCCCCAGCTA 111
         ||||  ||| ||||| | |||||||||||||||| |||||||||    ||||||| ||||||| ||||| ||
Db   299 ACTTCCTTTAGGGAAGTCCCTTCCAAGAGAAGAAGATGACTGCGGGGAGACAACCCCAGCTA 358

Qy   112 GTCCCAGCAGGACCAGGTGAACATTACAGAAATTTACAACAAGTCTCTTCTCGTCCTTCAAG 171
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   359 GTCCCAGCAGGACCAGGTGAACATTACAGAAATTTACAACAAGTCTCTTCTCGTCCTTCAAG 418

Qy   172 GAGAATGAGGAGAGAACATCCAGTGTGGGGAGGAACTTCAGTGGACAATAGAGTGTTTCATGGTC 231
         |||||||||||| ||||||||||||||||||||||||||| |||||||||||||||||||||||
Db   419 GAGAATGAGGAGGAACATCCAGTGTGGGGAGGAACTTCAGTGGACAATAGAGTGTTTCATGGTC 478

Qy   232 CTGAACCCCAGCCAGCAGCTGGCCATTGCAGTCCTGTCCCTCACGCGTGGGCGCACCTTCACG 291
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   479 CTGAACCCCAGCCAGCAGCTGGCCATTGCAGTCCTGTCCCTCACGCGTGGGCGCACCTTCACG 538

Qy   292 GTCCTCGGAGAACCTCCTCGGGTGCTGTGGGTCATCCTCACTCACTCCCGCGCCTCCGCGCTGCAGG 351
         ||||| |||||||||||||||||||||||||  |||||||||||||||||||||||||||||||||
Db   539 GTCCTGTGA 1567
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Query Match       95.3%;   Score 1257.8;   DB 13;   Length 5480;
Best Local Similarity   99.4%;   Pred. No. 0;
Matches 1262;   Conservative 0;   Mismatches 7;   Indels 0;   Gaps 0;

Qy    52  ACTGAACCTCCTGGGAAGTCCCTTCCAAGAGAAGAGAATGACTGCGGGGAGACAACCCCAGCTA  111
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Db   214  ACTTCCTTTAGGGGGGAAGTCCCTTCCAAGAGAAGAGAATGACTGCGGGGAGACAACCCCAGCTA  273

Qy   112  GTCCCAGCAGACCAGGTGAAACATTACAGAATTTATACAACAGTTCATGGGAGATGTTTTCAAG  171
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   274  GTCCCAGCAGACCAGGTGAAACATTACAGAATTTATACAACAGTTCATGGGAGATGTTTTCAAG  333

Qy   172  GAGAATGACGAGAACATCCAGTGTGGGGAGAACTTCATGGACATAGAGTGTTTTCAGG  231
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   334  GAGAATGACGAGAACATCCAGTGTGGGGAGAACTTCATGGACATAGAGTGTTTTCAGG  393

Qy   232  CTGAACCCCAGCCAGCAGCTGGCCATTGCAGTCGCCTGTCCCCTCACGCTGGGGCACCTTCACG  291
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   394  CTGAACCCCAGCCAGCAGCTGGCCATTGCAGTCGCCTGTCCCCTCACGCTGGGGCACCTTCACG  453

Qy   292  GTCCTGGAGAACCTCCTGGTGTGCGTGCGTGGGGCATCCTCCACTCCACTCCCGGCAGG  351
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   454  GTCCTGGAGAACCTCCTGGTGTGCGTGCGTGGGGCATCCTCCACTCCACTCCCGGCAGG  513

Qy   352  CCTTCCTACCACTTCATCGGCGACCTGGCGGTGGCAGACCTCCTGGGGGAGTGCATTTTT  411
          |||||||||||||||||||||||||||||||||||||||||||||||||
Db   514  CCTTCCTACCACTTCATCGGCGACCTGGCGGTGGCAGACCTCCTGGGGGAGTGCATTTTT  573

Qy   412  GTCTACAGCTTCATTGACTTCCACGTGTTCCACCGCAAAGATAGCCGCAAGTGTTTCTG  471
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   574  GTCTACAGCTTCATTGACTTCCACGTGTTCCACCGCAAAGATAGCCGCAAGTGTTTCTG  633

Qy   472  TTCAAAACTGGGGTGGGGTCACCGGCCTCCTTCACTGACCTGCCGCCTGTTCCTCACA  531
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   634  TTCAAAACTGGGGTGGGGTCACCGGCCTCCTTCACTGACCTGCCGCCTGTTCCTCACA  693

Qy   532  GCCATCGACAGGTACATATCCATTCACAGGCCCCTGGCCTATAAGAGGATTGTCACCAGG  591
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   694  GCCATCGACAGGTACATATCCATTCACAGGCCCCTGGCCTATAAGAGGATTGTCACCAGG  753

Qy   592  CCCAAGGCCGTGGTTGGGTTTTGCCTGATGTGGACCATAGCCATTGTGATCGCCGTGCTG  651
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   754  CCCAAGGCCGTGGTTGGGTTTTGCCTGATGTGGACCATAGCCATTGTGATCGCCGTGCTG  813

Qy   652  CCTCTCCTGGGCTGGAACTGCAAATCTGTTTGCTCAGACATTTTCCCACAC  711
          |||||||||||||||||||||||||||||||||||||||||||
Db   814  CCTCTCCTGGGCTGGAACTGCAAATCTGTTTGCTCAGACATTTTCCCACAC  873

Qy   712  ATTGATGAAAACCTACCTGATGTTCTGGATCGGGGGTCACCAGCCTTCATC  771
          |||||||||||||||||||||||||||||||||||||||||||
Db   874  ATTGATGAAAACCTACCTGATGTTCTGGATCGGGGGTCACCAGCCTTCATC  933

Qy   772  GTGTATGGGTACATGTATATTCTCTGGAAGGCTCACAGCCACGCCGCCGTGCCGATGATTCAG  831
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   772  GTGTATGGGTACATGTATATTCTCTGGAAGGCTCACAGCCACGCCGCCGTGCCGATGATTCAG  831
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Db   539  GTCCTGGAGAACCTCCTGGTGTGCGTGCGTGGGGCATCCTCCACTCCACTCCCGGCAGG  598
Qy   352  CCTTCCTACCACTTCATCGGCGACCTGGCGGTGGCAGACCTCCTGGGGGAGTGCATTTTT  411
Db   599  CCTTCCTACCACTTCATCGGCGACCTGGCGGTGGCAGACCTCCTGGGGGAGTGCATTTTT  658
Qy   412  GTCTACAGCTTCATTGACTTCCACGTGTTCCACCGCAAAGATAGCCGCAAGTGTTTCTG  471
Db   659  GTCTACAGCTTCATTGACTTCCACGTGTTCCACCGCAAAGATAGCCGCAAGTGTTTCTG  718
Qy   472  TTCAAAACTGGGGTGGGGTCACCGGCCTCCTTCACTGACCTGCCGCCTGTTCCTCACA  531
Db   719  TTCAAAACTGGGGTGGGGTCACCGGCCTCCTTCACTGACCTGCCGCCTGTTCCTCACA  778
Qy   592  CCCAAGGCCGTGGTTGGGTTTTGCCTGATGTGGACCATAGCCATTGTGATCGCCGTGCTG  651
Db   779  GCCATCGACAGGTACATATCCATTCACAGGCCCCTGGCCTATAAGAGGATTGTCACCAGG  838
Qy   532  GCCATCGACAGGTACATATCCATTCACAGGCCCCTGGCCTATAAGAGGATTGTCACCAGG  591
Db   839  CCCAAGGCCGTGGTTGGGTTTTGCCTGATGTGGACCATAGCCATTGTGATCGCCGTGCTG  898
Qy   652  CCTCTCCTGGGCTGGAACTGCAAATCTGTTTGCTCAGACATTTTCCCACAC  711
Db   899  CCTCTCCTGGGCTGGAACTGCAAATCTGTTTGCTCAGACATTTTCCCACAC  958
Qy   712  ATTGATGAAAACCTACCTGATGTTCTGGATCGGGGGTCACCAGCCTTCATC  771
Db   959  ATTGATGAAAACCTACCTGATGTTCTGGATCGGGGGTCACCAGCCTTCATC  1018
Qy   772  GTGTATGGGTACATGTATATTCTCTGGAAGGCTCACAGCCACGCCGCCGTGCCGATGATTCAG  831
Db  1019  GTGTATGGGTACATGTATATTCTCTGGAAGGCTCACAGCCACGCCGCCGTGCCGATGATTCAG  1078
Db   832  CGTGGGCACCCAGAAGAGCAATCATCATCCAACAGCTTCTGAGGATGGGAGGTACAGGTGACC  891
Db  1079  CGTGGGCACCCAGAAGAGCAATCATCATCCAACAGCTTCTGAGGATGGGAGGTACAGGTGACC  1138
Qy   892  CGGCCAGACCAAGCCCCGCATGGACATTAGGTTAGCCAAGACCCTGGTCCTGATCCTGGTG  951
Db  1139  CGGCCAGACCAAGCCCCGCATGGACATTAGGTTAGCCAAGACCCTGGTCCTGATCCTGGTG  1198
Qy   952  GTGTTGATCATCTGCTGGGGCCCTCTGCTTGCAATCATGGTGTATGATGTCTTTGGGAAG  1011
Db  1199  GTGTTGATCATCTGCTGGGGCCCTCTGCTTGCAATCATGGTGTATGATGTCTTTGGGAAG  1258
Qy  1012  ATGAACAAGCTCATTAAGACGGTGTTTGCATTCTGCAGTATGCTGTGCCTGCTGAACTCC  1071
Db  1259  ATGAACAAGCTCATTAAGACGGTGTTTGCATTCTGCAGTATGCTGTGCCTGCTGAACTCC  1318
Qy  1072  ACCGTGAACCCCATCATCTATGCTCTGAGGAGTAAAGAACACCTGCGACAGGTGTTTCTG  1131
Db  1319  ACCGTGAACCCCATCATCTATGCTCTGAGGAGTAAAGAACACCTGCGACAGGTGTTTCTG  1378
Qy  1132  ATGTTTCCCTCTTGTGAAGGCACTGCGCAGCCTCTCGATAAACAGCACTGGGGGACTCGGAC  1191
Db  1379  ATGTTTCCCTCTTGTGAAGGCACTGCGCAGCCTCTCGATAAACAGCACTGGGGGACTCGGAC  1438
Qy  1192  TGCCTGCACAAACACGCAAACAATGCAGCCAGTGTCCAGGCCGCCGAGAAAAGCTGCATC  1251
Db  1439  TGCCTGCACAAACACGCAAACAATGCAGCCAGTGTCCAGGCCGCCGAGAAAAGCTGCATC  1498
Qy  1252  AAGAGCACGGTCAAGATTGCCAAGGTAACCAAGTCTCTGTCCAGAGACACGTCTGCCGAG  1311
Db  1499  AAGAGCACGGTCAAGATTGCCAAGGTAACCAAGTCTCTGTGTCCAGAGACACGTCTGCCGAG  1558
Qy  1312  GCTCTCTGTGA  1320
Db  1559  GCTCTCTGTGA  1567
Qy  1499  AAGAGCACGGTCAAGATTGCCAAGGTAACC
Db  1567
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RESULT 9
US-10-208-408-52
; Sequence 52, Application US/10208408
; Publication No. US20030096272A1
; GENERAL INFORMATION:
; APPLICANT: Schebye, Xiao Min
; TITLE OF INVENTION: GENES REGULATED BY PEROXISOME PROLIFERATOR-ACTIVATED RECEPTOR
; FILE REFERENCE: PA-0048-1 US
; CURRENT APPLICATION NUMBER: US/10/208,408
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 60/308,868
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PERL Program
; SEQ ID NO 52
; LENGTH: 5653
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030096272A1 13837759.1
US-10-208-408-52

Query Match     95.3%;  Score 1257.8;  DB 6;  Length 5653;
Best Local Similarity   99.4%;  Pred. No. 0;  Mismatches 7;  Indels 0;  Gaps 0;
Matches 1262;  Conservative   0;  Mismatches 7;  Indels 0;  Gaps 0;
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The remaining content consists of paired nucleotide sequence alignment blocks (Qy / Db) with matching bars, e.g.:

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Qy    112  GTCCCAGCAGACCAGGTGAACATTACAGAATTTACACAAGTCTCTCGTCCTTCAAG  171
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Db    112  GTCCCAGCAGACCAGGTGAACATTACAGAATTTACACAAGTCTCTCGTCCTTCAAG  171

Qy    52   ACTGACCTCCTGGGAAGTCCCTTCCAAGAGAAGAATGACTGGCGGGAGACAACCCCCAGCTA  111
           ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    260  ACTTCCTTTAGGGGAAGTCCCCTTCCAAGAGAAGAATGACTGGCGGGACAACCCCCAGCTA  319
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(The full page continues with many such aligned Qy/Db sequence pairs, positions 112 through 1482 on the left column and 320 through 1459 on the right column.)

RESULT 10
US-10-521-420-2
; Sequence 2, Application US/10521420
; Publication No. US20050239133A1
; GENERAL INFORMATION:
; APPLICANT: Greasley, Peter
; TITLE OF INVENTION: Methods to Identify True Antagonists and Inverse Agonists of the
; TITLE OF INVENTION: Cannabinoid Receptor
; FILE REFERENCE: A52D-P01-752
; CURRENT APPLICATION NUMBER: US/10/521,420
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: SE 0202242-4
; PRIOR FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1419
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-521-420-2

Query Match   95.2%; Score 1256.2; DB 10; Length 1419;
Best Local Similarity   99.4%; Pred. No. 0; Mismatches 8; Indels 0; Gaps 0;
Matches 1261; Conservative   0; Mismatches 8; Indels   0; Gaps   0;

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Qy     52 ACTGACCTCCTGGGAAGTCCCTTCCAAGAGAAGAGATGACTGCGGGAGGAGACAACCCCAGCTA 111
          ||||| || ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    151 ACTTCCTTTAGGGAGAACCTCCTGGTGCGTGGCTCATCCTCCACTCCCGCTCCGCGCACCTTCACG 210

Qy    112 GTCCCAGCAGACAGCCAGGTGAACATTACAGAATATTTACAACACAGTCTCTTCTCTCCTTCAAG 171
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    211 GTCCCAGCAGACCAGGTGAACATTACAGAATTTTACAACACAAGTCTCTTCTCTCGTCCTTCAAG 270

Qy    172 GAGAATGAGGAGGAACATTCCAGTGTGGGGGAGAACTTCATTGGACATAGAGTGTTTCATGGTC 231
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    271 GAGAATGAGGAGGAACATTCCAGTGTGGGGGAGAACTTCATTGGACATAGAGTGTTTCATGGTC 330

Qy    232 CTGAACCCCAGCCAGCAGCTGGCCATTGCCAGTCCCGTGGGCCACCTTCACG 291
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    331 CTGAACCCCAGCCAGCAGCTGGCCATTGCAGTCCCGTGTCCCGCGCACCTTCACG 390

Qy    292 GTCCTGGAGAGACCTCCTGGGTGTCGGTCATCCTCCACTCCCGCTCCGCTGCAGG 351
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    391 GTCCTGGAGAACCTCCTGGGTGTGGGCGTCATCCTCCACTCCCGCTCCGCTGCAGG 450

Qy    352 CCTTCCTTACCACTCATCGGCAGCCTGGCCTGCCTCCTGGGGAGTGGTCATTTT 411
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    451 CCTTCCTTACCACTCATCGGCAGCCTGGGGGCGGCTGGCCTGGGGAGTGGTCATTTT 510

Qy    412 GTCCTACAAGCTTCATTGACTTCCACGTGTTCCACCGCAAAGATAGCCCGAACCGTGTTTCTG 471
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    511 GTCTACAAGCTTCATTGACTTCCACGTGTTCCACCGCAAAGATAGCCCGAACGTGTTTCTG 570

Qy    472 TTCAAACTGGGTGGGGTCACGGCCCTCCTTCACTGCCTCCGTGTTCCTCACA 531
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    571 TTCAAACTGGGTGGGGTCACGGCCCTCCTTCACTGCCTCCGTGTTCCTCACA 630

Qy    532 GCCATCGACAGGTACATATCCATTCAATTCACAGGCCCTCTGAAGAGGATTGTCACCAGG 591
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    631 GCCATCGGCAGTACATATCCATTCAATTCACAGGCCCCTGTAAGAGGATTGTCACCAGG 690

Qy    592 CCCAAGGCCGTGGTAGGGTTTGCCTGATGTGGACCATAGCCATTGTGATCGCCGTGCTG 651
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    651 ...

Qy   1252 AAGAGCACGGTCAAGATTGGCCAAGGTAACCACTGTCTGTTGTCCACAGAGACACGGTCTGCCGAG 1311
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1460 AAGAGCACGGTCAAGATTGGCCAAGGTAACCACTGTCTGTTGTCCACAGAGACACGGTCTGCCGAG 1519

Qy   1312 GCTCTGTGA 1320
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Db   1520 GCTCTGTGA 1528
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RESULT 11
US-10-521-420-3
; Sequence 3, Application US/10521420
; Publication No. US20050239133A1
; GENERAL INFORMATION:
; APPLICANT: Greasley, Peter
; TITLE OF INVENTION: Methods to Identify True Antagonists and Inverse Agonists of the
; TITLE OF INVENTION: Cannabinoid Receptor
; FILE REFERENCE: A52D-P01-752
; CURRENT APPLICATION NUMBER: US/10/521,420
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: SE 0202242-4
; PRIOR FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 1419
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-521-420-3

Query Match   95.2%; Score 1256.2; DB 10; Length 1419;

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Db    691 CCCAAGGCCGTGGTGCGGGTTTTGCCTGATGTGGACCATAGCCATTGTGATCGCCGTGCTG 750

Qy    652 CCTCCTCGGGCTGGAACTGGCGAGAAAACTGCAAACTGTGTTTGCTCAGACAATTTTCCCACAC 711
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    751 CCTCCTCGGGCTGGAACTGGCGAGAAAACTGCAAACTGTGTTTGCTCAGACAATTTTCCCACAC 810

Qy    712 ATTGGATGAAAACCTACCTGATGTGTTCTGGATCGGGGGTCACCAGCGGTCACCAGCGTTCTGTTCATC 771
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    811 ATTGGATGAAAACCTACCTGATGTGTTCTGGATCGGGGTCACCAGCGGTCACCAGCGTTCTGTTCATC 870

Qy    772 GTGTATGCGTACATGTATATTCTCTGGAAGGCTCACAGCCCACGCCGCCGTCCGCATGATTCAG 831
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    871 GTGTATGCGTACATGTATATTCTCTGGAAGGCTCACAGCCCACGCCGCCGTCCGCATGAATTCAG 930

Qy    832 CGTCGGCACCCAGGAGAGCAATCATCATCCACACGTCTGAGGATGGGAAGGTACAGGTGACC 891
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    931 CGTCGGCACCCAGGAGAGCAATCATCATCCACACGTCTGAGGATGGGAAGGTACAGGTGACC 990

Qy    892 CGGCCAGACCAAGCCCGCATGGACATTAGGTTAGCCAAGAACCCCTGGTCCTGGATCCTGTGTG 951
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    991 CGGCCAGACCAAGCCCGCATGGACATTAGGTTAGCCAAGAACCCCTGGTCCTGGATCCTGTGTG 1050

Qy    952 GTGTTGATCATCTGCTGGGGCCCCTTCTTCTTGCTGTTGCAATCATCGGTGTATGATGAGTCTTTGGAG 1011
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1051 GTGTTGATCATCTGCTGGGGCCCCTTCTTCTTGCTGTTGCAATCATCGGTGTATGATGAGTCTTTGGAG 1110

Qy   1012 ATGAACAAGCTCATTAAGAGCGGTGTTTGCATTCTGCAGTATGCTCCTGTCCTGAAACTCC 1071
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1111 ATGAACAAGCTCATTAAGAGCGGTGTTTGCATTCTGCAGTATGCTCCTGTCCTGAAACTCC 1170

Qy   1072 ACCGGTGAACCCCATCACTCTATCTGCTCGGAGGTAAGGACCTGCGGCGACAGCGCTTTCCGGAGC 1131
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1171 ACCGTGACCCATCACTCTATGCTTCTGAGGAGTAAGGACACTGCCACAGCGCTTTCCGGGAC 1230

Qy   1132 ATGTTTCCCTCTTGTTGGAAGGGCACTGCGGCCAGCCTCCTGGAATAACAGCATGGGGGGACTGGAC 1191
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1231 ATGTTTCCCTCTTGTTGGAAGGGCACTGCGGCCAGCCTCCTGGAATAACAGCATGGGGGACTGGAC 1290

Qy   1192 TGCCTGCACAAAACACGCAAAACAATGCAGCCAGTTCTTCACAGCGGCCGCAGAAAAGCTGCATC 1251
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1291 TGCCTGCACAAAACACGCAAAACAATGCAGCCAGTTCTTCACAGCGGCCGCAGAAAAGCTGCATC 1350

Qy   1252 AAGAGCACGGTCAAGATTGCCAAGGTAACCAGTGTCTGTTGTCCACAGAGACACGGTCTGCCGAG 1311
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1351 AAGAGCACGGTCAAGATTGCCAAGGTAACCAGTGTCTGTTGTCCACAGAGACACGGTCTGCCGAG 1410

Qy   1312 GCTCTGTGA 1320
          |||||||||
Db   1411 GCTCTGTGA 1419
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Best Local Similarity 99.4%; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Matches 1261;

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Qy     52 ACTGACCTCCTGGGAAGTCCCTTCCAAGAGAAGAGATGACTGCGGGAGGAGCAACCCCCAGCTA 111
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    151 ACTTCCTTTAGGGAAGTCCCTTCCAAGAGAAGAGATGACTGCGGGAGGAGCAACCCCCAGCTA 210

Qy    112 GTCCCAGCGACGACCAGGTGAACATTACAGAAATTTTACAACAAGTCTCTTCGTCCTTCAAG 171
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    211 GTCCCAGCGACGACCAGGTGAACATTACAGAAATTTTACAACAAGTCTCTTCGTCCTTCAAG 270

Qy    172 GAGAATGAGGAGAACATCCAGTGTGGGGAGAACTTCATGGACATAGAGTGTTTCATGGTC 231
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    271 GAGAATGAGGAGAACATCCAGTGTGGGGAGAACTTCATGGACATAGAGTGTTTCATGGTC 330

Qy    232 CTGAACCCCAGCCAGCCAGCTGCCATTGCAGTCCTGTTCCCTCACGCCACCTTCACG 291
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    331 CTGAACCCCAGCCAGCCAGCTGGCCATTGCAGTCCTGTTCCCTCACGCCACCTTCACG 390

Qy    292 GTCCTGGAGAACCTCCTGGGTGCTGGGTGGGGTCAGCCTGCAGG 351
          ||||||||||||||||||||||||||||||||||||||||||||
Db    391 GTCCTGGAGAACCTCCTGGGTGCTGGGTGGGGTCAGCCTGCAGG 450

Qy    352 CCTTCCTACCCACTTCATCGGGCAGCCCTGGCGTGGGCAGACCTCCTGGGGAGTGTGCATTTTT 411
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    451 CCTTCCTACCCACTTCATCGGGCAGCCCTGGCGTGGGCAGACCTCCTGGGGAGTGTGCATTTTT 510

Qy    412 GTCTACAGCTTCATTGACTTCACGTGTTCCACGCGAAAGATAGCCCCAACGTGTTTCTG 471
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    511 GTCTACAGCTTCATTGACTTCACGTGTTCCACGCGAAAGATAGCCCCAACGTGTTTCTG 570

Qy    472 TTCAAACTGGGGTGGGGGTTCACGGCCTCCTTCACTGCCTTCCGTGGGCAGCCTGTTCCTCACA 531
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    571 TTCAAACTGGGGTGGGGGTTCACGGCCTCCTTCACTGCCTTCCGTGGGCAGCCTGTTCCTCACA 630

Qy    532 GCCATCGACAGGTACATATCCATTCACAGGCCCTGGGCCTATAAAGAGGATTGTTCACCAGG 591
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    631 GCCATCGACAGGTACATATCCATTCACAGGCCCTATAAAGAGGATTGTTCACCAGG 690

Qy    592 CCCAAGCCCGTGGTAGGCGTTTTGCCTGATTGTGATCGCCGTGCTG 651
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    691 CCCAAGGCCGTGGTGGCGCTTTTGCCCTGATTGTGATCGGCCGTGCTG 750

Qy    652 CCTCTCCTGGGCTGGAACTGCGAAATCTCGTTTTGCTCAGACATTTTTCCCACAC 711
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    751 CCTCTCCTGGGCTGGAACTGCGAAATCTCGTTTTGCTCAGACATTTTTCCCACAC 810

Qy    712 ATTGATGAAACCTACCTGAGTTCTGGAATCGGGGGTCACCGGCTACTCGTTGTTCATC 771
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    811 ATTGATGAAACCTACCTGAGTTCTGGAATCGGGGGTCACCGGCTACTCGTTGTTCATC 870

Qy    772 GTGTATGGTACATGTATATTCTCTGGAGAGGGTCACAGCCACGTCCGCTCGTTGTTCATCAG 831
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    871 GTGTATGGGTACAGTGTATATTCTCTGGAAGGGTCACAGCCACGTCCGCTCGTTGTTCAG 930

Qy    832 CGTGGCACCCAGAAGAGAGAGATCATCATCCACACACTCTCGAGGATGGGAAGGTACAGGTGACC 891
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    931 CGTGGCACCCAGAAGAGAGAGAGATCATCATCACCTCGAGGATGGGAAGGTACAGGTGACC 990

Qy    892 CGGCCAGACCAAGCCCCGCACTGGACATTAGGTTAGCCAAGACCCTGGTCCTGATCCTGGTG 951
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    991 CGGCCAGACCAAGCCCCCATGGCCATTAGGTTAGCCAAGACCCTGGTCCTGATCCTGGTG 1050

Qy    952 GTGTTGATCATCTGCTGGGGCCCCTTCGCTTGCAATCATGGTGTATGATGCTTGGGAAG 1011
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1051 GTGTTGATCATCTGCTGGGGGCCCCTTCGCTTGCAATCATGGTGTATGATGCTTGGGAAG 1110

Qy   1012 ATGAACAAGCTCATTAAGACGGGTGTTTCCATTCTGCAGTATGGTTCTGCTGCTGAACTCC 1071
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1111 ATGAACAAGCTCATTAAGACGGGTGTTTCCATTCTGCAGTATGGTTCTGCTGCTGAACTCC 1170

Qy   1072 ACCGTGAACCCCATCATCTTATGCTCTGAGGAGTAAGAGGACCTGCCACAGGCCTTTCCGGAGC 1131
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1131 ACCGTGAACCCCATCATCTTATGCTCTGAGGAGTAAGAGGACCTGCCACAGGCCTTTCCGGAGC 1131
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Db   1171 ACCGTGAACCCCATCATCTTATGTCTCTGAGGAGTAAGAGGACCTCCGACACGGCTTTCCGGAGC 1230
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1132 ATGTTTTCCCTCTTGTGGAAGGCACTGCGGCGCCGCTTCTCTGGGATAACAGCATGGGGGGACTCGGAC 1191
Db   1231 ATGTTTTCCCTCTTGTGGAAGGCACTGCGGCGCCGCTTCTCTGGGATAACAGCATGGGGGGACTCGGAC 1290
Db   1192 TGGCTGCACAAAACACGCAAAACAATGCAGCCCACTGTTCACAGGGCCCCAGGAAAAGCTGCATC 1251
Db   1291 TGGCTGCACAAAACACGCAAAACAATGCAGCCCACTGTTCACAGGGCCCCAGGAAAAGCTGCATC 1350
Db   1252 AAGAGCACGGTCAAGATTGCCAAGGGTAACCACTGTCTGTTGTGTCCACAGACAGCACGTTGCCGAG 1311
Db   1351 AAGAGCACGGTCAAGATTGCCAAGGGTAACCACTGTCTGTTGTGTCCACAGACAGCACGTTGCCGAG 1410
Db   1312 GCTTCTGTGA 1320
Db   1411 GCTTCTGTGA 1419
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RESULT 12
US-10-101-510-715
; Sequence 715, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
; APPLICANT: WAN, JACKSON
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
; FILE REFERENCE: 15117.0012
; CURRENT APPLICATION NUMBER: US/10/101,510
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/276,947
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 805
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 715
;   LENGTH: 2135
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-101-510-715

Query Match   95.2%;
Best Local Similarity   99.4%; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Matches 1261; Score 1256.2; DB 7; Length 2135;

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Qy     52 ACTGACCTCCTGGGAAGTCCCTTCCAAGAGAAGAGATGACTGCGGGAGGAGCAACCCCCAGCTA 111
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    242 ACTTCCTTTAGGGAAGTCCCTTCCAAGAGAAGAGATGACTGCGGGAGGAGCAACCCCCAGCTA 301

Qy    112 GTCCCAGCGACGACCAGGTGAACATTACAGAAATTTTACAACAAGTCTCTTCGTCCTTCAAG 171
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    302 GTCCCAGCGACGACCAGGTGAACATTACAGAAATTTTACAACAAGTCTCTTCGTCCTTCAAG 361

Qy    172 GAGAATGAGGAGAACATCCAGTGTGGGGAGAACTTCATGGACATAGAGTGTTTCATGGTC 231
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    362 GAGAATGAGGAGAACATCCAGTGTGGGGAGAACTTCATGGACATAGAGTGTTTCATGGTC 421

Qy    232 CTGAACCCCAGCCAGCCAGCTGGCCATTGCAGTCCTGTTCCCTCACGCCACCTTCACG 291
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    422 CTGAACCCCAGCCAGCCAGCTGGCCATTGCAGTCCTGTTCCCTCACGCCACCTTCACG 481

Qy    292 GTCCTGGAGAACCTCCTGGGTGTGGGTGCGTCATCCTGCAGG 351
          ||||||||||||||||||||||||||||||||||||||||||
Db    482 GTCCTGGAGAACCTCCTGGGTGTGGCTGTGCGTCATCCTGCAGG 541

Qy    352 CCTTCCTACCCACTTCATCGGCAGCCCTGGCGCGGTGGCAGACCTCCTGGGGAGTGTGCATTTTT 411
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    542 CCTTCCTACCCACTTCATCGGCAGCCCTGGCGCGGTGGCAGACCTCCTGGGGAGTGTGCATTTTT 601

Qy    412 GTCTACAGCTTCATTGACTTCACGTGTTCCACGCGAAAGATAGCCCGAACGTGTTTCTG 471
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    602 GTCTACAGCTTCATTGACTTCCACGTGTTCCACGCGCAAAGATAGCCCGAACGTGTTTCTG 661

Qy    472 TTCAAACTGGGGTGGGGGTCACGGCCTCCTTCACTGCCTTCCGTGGGCAGCCTGTTCCTCACA 531
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    662 TTCAAACTGGGGTGGGGGTCACGGCCTCCTTCACTGCCTTCCGTGGGCAGCCTGTTCCTCACA 531
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; SOFTWARE: PERL Program
; SEQ ID NO 1450
; LENGTH: 2135
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: GenBank ID No. US2004010136A1 9736236
US-10-305-720-1450

Query Match        95.2%;   Score 1256.2;  DB 7;  Length 2135;
Best Local Similarity   99.4%;   Pred. No. 0;
Matches 1261; Conservative   0; Mismatches   8; Indels   0; Gaps   0;

Qy     52 ACTGACCTCCTGGGAAGTCCCTTCCAAGAAGAAGTGACGGGGAGAAGACATGGCACACAGCTA 111
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    242 ACTTCCTTTAGGGGAAGTCCCTTCCAAGAAGAAGGAAGAGTGACGGGGAGAAGACCCAGCTA 301

Qy    112 GTCCCCAGCGAGACCAGCAGGTGAGAACATTACAGAAATTTTACAACAAGTCTCTCTCGGTCCTTCAAG 171
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    302 GTCCCCAGCAGACCAGGTGAACATTACAGAAATTTTACAACAAGTCTCTCTCGGTCCTTCAAG 361
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Qy         952 GTGTTGATCATCTGCTGGGGCCCTCTGCTTGCAATCATGGTGTATGATGTCTTTGGGAAG 1011
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1142 GTGTTGATCATCTGCTGGGGCCCTCTGCTTGCAATCATGGTGTATGATGTCTTTGGGAAG 1201

Qy        1012 ATGAACAAGCTCATTAAGACGGTGTTTGCATTCTGCAGTATGCTCTGCCTGCTGAACTCC 1071
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1202 ATGAACAAGCTCATTAAGACGGTGTTTGCATTCTGCAGTATGCTCTGCCTGCTGAACTCC 1261

Qy        1072 ACCGTGAACCCCATCATCTATGCTCTGAGGAGTAAGGACCTGCGACACGCTTTCCGGAGC 1131
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1262 ACCGTGAACCCCATCATCTATGCTCTGAGGAGTAAGGACCTGCGACACGCTTTCCGGAGC 1321

Qy        1132 ATGTTTCCCTCTTGTGAAGGCACTGCGCAGCCTCTGGATAACAGCATGGGGGACTCGGAC 1191
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1322 ATGTTTCCCTCTTGTGAAGGCACTGCGCAGCCTCTGGATAACAGCATGGGGGACTCGGAC 1381

Qy        1192 TGCCTGCACAAACACGCAAACAATGCAGCCAGTGTTCACAGGGCCGCAGAAAGCTGCATC 1251
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1382 TGCCTGCACAAACACGCAAACAATGCAGCCAGTGTTCACAGGGCCGCAGAAAGCTGCATC 1441

Qy        1252 AAGAGCACGGTCAAGATTGCCAAGGTAACCATGTCTGTGTCCACAGACACGTCTGCCGAG 1311
               |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1442 AAGAGCACAGTCAAGATTGCCAAGGTAACCATGTCTGTGTCCACAGACACGTCTGCCGAG 1501

Qy        1312 GCTCTGTGA 1320
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Db        1502 GCTCTGTGA 1510

RESULT 14
US-10-641-643-1469
; Sequence 1469, Application US/10641643
; Publication No. US20040077003A1
;   GENERAL INFORMATION:
;        APPLICANT: Cocks, Benjamin G.
;                   Susan G. Stuart
;                   Jeffrey J. Seilhamer
;        TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
;                            GENE EXPRESSION
;        NUMBER OF SEQUENCES: 1508
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
;             STREET: 3174 PORTER DRIVE
;             CITY: PALO ALTO
;             STATE: CALIFORNIA
;             COUNTRY: USA
;             ZIP: 94304
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/641,643
;             FILING DATE: 14-Aug-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: <Unknown>
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Zeller, Karen J.
;             REGISTRATION NUMBER: 37,071
;             REFERENCE/DOCKET NUMBER: PA-0001 US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (650) 855-0555
;             TELEFAX: (650) 845-4166
;   INFORMATION FOR SEQ ID NO: 1469:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2135 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
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;        IMMEDIATE SOURCE:
;             LIBRARY: GENBANK
;             CLONE: g736236
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1469 :
US-10-641-643-1469

  Query Match             95.2%;  Score 1256.2;  DB 8;  Length 2135;
  Best Local Similarity   99.4%;  Pred. No. 0;
  Matches 1261;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          52 ACTGACCTCCTGGGAAGTCCCTTCCAAGAGAAGATGACTGCGGGAGACAACCCCCAGCTA 111
               |||  | |   |||||||||||||||||||||||||||||||||||||||||||||||||
Db         242 ACTTCCTTTAGGGGAAGTCCCTTCCAAGAGAAGATGACTGCGGGAGACAACCCCCAGCTA 301

Qy         112 GTCCCAGCAGACCAGGTGAACATTACAGAATTTTACAACAAGTCTCTCTCGTCCTTCAAG 171
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         302 GTCCCAGCAGACCAGGTGAACATTACAGAATTTTACAACAAGTCTCTCTCGTCCTTCAAG 361

Qy         172 GAGAATGAGGAGAACATCCAGTGTGGGGAGAACTTCATGGACATAGAGTGTTTCATGGTC 231
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         362 GAGAATGAGGAGAACATCCAGTGTGGGGAGAACTTCATGGACATAGAGTGTTTCATGGTC 421

Qy         232 CTGAACCCCAGCCAGCAGCTGGCCATTGCAGTCCTGTCCCTCACGCTGGGCACCTTCACG 291
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         422 CTGAACCCCAGCCAGCAGCTGGCCATTGCAGTCCTGTCCCTCACGCTGGGCACCTTCACG 481

Qy         292 GTCCTGGAGAACCTCCTGGTGCTGTGCGTCATCCTCCACTCCCGCAGCCTCCGCTGCAGG 351
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         482 GTCCTGGAGAACCTCCTGGTGCTGTGCGTCATCCTCCACTCCCGCAGCCTCCGCTGCAGG 541

Qy         352 CCTTCCTACCACTTCATCGGCAGCCTGGCGGTGGCAGACCTCCTGGGGAGTGTCATTTTT 411
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         542 CCTTCCTACCACTTCATCGGCAGCCTGGCGGTGGCAGACCTCCTGGGGAGTGTCATTTTT 601

Qy         412 GTCTACAGCTTCATTGACTTCCACGTGTTCCACCGCAAAGATAGCCGCAACGTGTTTCTG 471
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         602 GTCTACAGCTTCATTGACTTCCACGTGTTCCACCGCAAAGATAGCCGCAACGTGTTTCTG 661

Qy         472 TTCAAACTGGGTGGGGTCACGGCCTCCTTCACTGCCTCCGTGGGCAGCCTGTTCCTCACA 531
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         662 TTCAAACTGGGTGGGGTCACGGCCTCCTTCACTGCCTCCGTGGGCAGCCTGTTCCTCACA 721

Qy         532 GCCATCGACAGGTACATATCCATTCACAGGCCCCTGGCCTATAAGAGGATTGTCACCAGG 591
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         722 GCCATCGACAGGTACATATCCATTCACAGGCCCCTGGCCTATAAGAGGATTGTCACCAGG 781

Qy         592 CCCAAGGCCGTGGTAGCGTTTTGCCTGATGTGGACCATAGCCATTGTGATCGCCGTGCTG 651
               |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db         782 CCCAAGGCCGTGGTGGCGTTTTGCCTGATGTGGACCATAGCCATTGTGATCGCCGTGCTG 841

Qy         652 CCTCTCCTGGGCTGGAACTGCGAGAAACTGCAATCTGTTTGCTCAGACATTTTCCCACAC 711
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         842 CCTCTCCTGGGCTGGAACTGCGAGAAACTGCAATCTGTTTGCTCAGACATTTTCCCACAC 901

Qy         712 ATTGATGAAACCTACCTGATGTTCTGGATCGGGGTCACCAGCGTACTGCTTCTGTTCATC 771
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         902 ATTGATGAAACCTACCTGATGTTCTGGATCGGGGTCACCAGCGTACTGCTTCTGTTCATC 961

Qy         772 GTGTATGCGTACATGTATATTCTCTGGAAGGCTCACAGCCACGCCGTCCGCATGATTCAG 831
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         962 GTGTATGCGTACATGTATATTCTCTGGAAGGCTCACAGCCACGCCGTCCGCATGATTCAG 1021

Qy         832 CGTGGCACCCAGAAGAGCATCATCATCCACACGTCTGAGGATGGGAAGGTACAGGTGACC 891
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1022 CGTGGCACCCAGAAGAGCATCATCATCCACACGTCTGAGGATGGGAAGGTACAGGTGACC 1081

Qy         892 CGGCCAGACCAAGCCCGCATGGACATTAGGTTAGCCAAGACCCTGGTCCTGATCCTGGTG 951
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1082 CGGCCAGACCAAGCCCGCATGGACATTAGGTTAGCCAAGACCCTGGTCCTGATCCTGGTG 1141

Qy         952 GTGTTGATCATCTGCTGGGGCCCTCTGCTTGCAATCATGGTGTATGATGTCTTTGGGAAG 1011
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Db        1142 GTGTTGATCATCTGCTGGGGCCCTCTGCTTGCAATCATGGTGTATGATGTCTTTGGGAAG 1201
```

RESULT 15
US-10-101-510-409
Sequence 409, Application US/10101510
Publication No. US20030148295A1
GENERAL INFORMATION:
APPLICANT: WAN, JACKSON
APPLICANT: WANG, YIXIN
TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
FILE REFERENCE: 15117.0012
CURRENT APPLICATION NUMBER: US/10/101,510
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: 60/276,947
PRIOR FILING DATE: 2001-03-20
SOFTWARE: Patentin Ver. 2.1
NUMBER OF SEQ ID NOS: 805
SEQ ID NO 409
LENGTH: 5651
TYPE: DNA
ORGANISM: Homo sapiens
US-10-101-510-409

Query Match   95.2%; Score 1256.2; DB 7; Length 5651;
Best Local Similarity   99.4%;
Matches 1261; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

[Sequence alignment of Query (Qy) against Database (Db), positions approximately 52–1528, presented as paired Qy/Db rows with alignment markers.]

Search completed: June 17, 2006, 00:20:06
Job time : 1647 secs

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